生物信息学数据库的检索与利用

何晓薇

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VISIT…

LANZAROTE Caliente.com

主要内容

- 生物信息学数据库的分类
- NCBI
  - 概况
  - Entrez
  - GenBank
  - My NCBI
  - Blast

生物信息学数据库的分类（1）

- 核酸序列数据库
- 蛋白质序列数据库
- 蛋白质结构数据库
- 基因组数据库

生物信息学数据库的分类（2）

- 一级数据库
- 二级数据库
- 专家库
- 整合数据库

核酸序列数据库

- 欧洲分子生物学实验室的EMBL

  http://www.embl-heidelberg.de

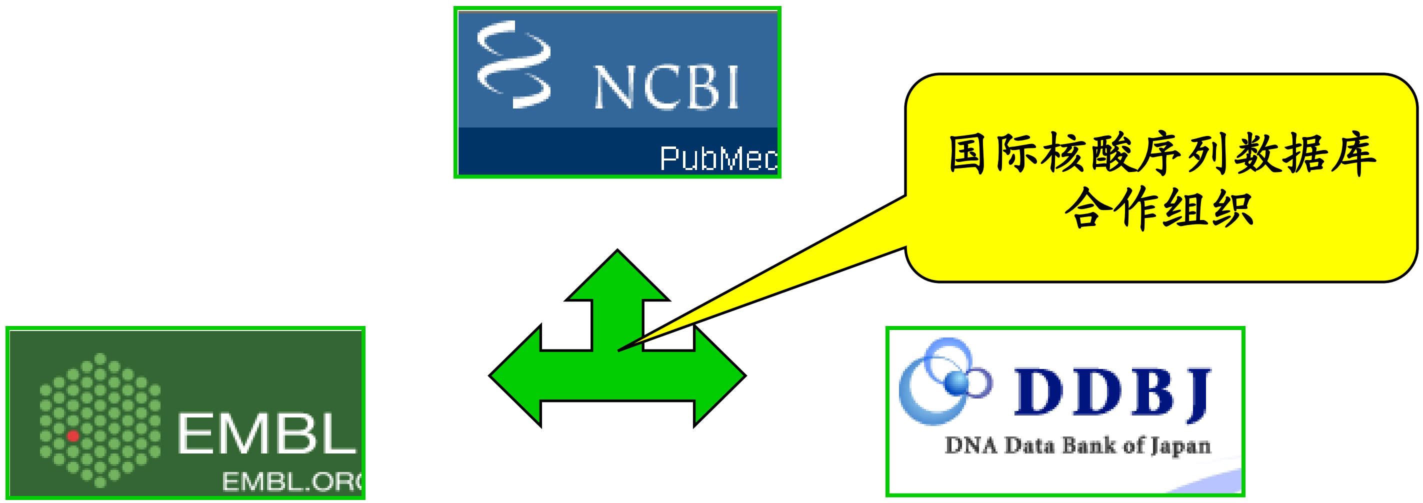
- 美国生物技术信息中心的GenBank

  http://www.ncbi.nlm.nih.gov/Genbank/

- 日本国立遗传研究所的DDBJ

  http://www.ddbj.nig.ac.jp/searches-e.html

国际上最权威的核酸序列数据库



- 数据每天交换
- Accession number、序列数据和注解相同

蛋白质序列数据库

- **SWISS-PROT** 蛋白质序列数据库

  http://www.expasy.ch/sprot/sprot-top.html

- **PIR** 蛋白质序列信息资源库

  http://pir.georgetown.edu/

- **PROSITE**

  http://au.expasy.org/prosite/

- **NCBI** 蛋白质数据库

  http://www.ncbi.nlm.nih.gov/entrez

蛋白质序列数据库

European Bioinformatics Institute

Protein Information Resource

Swiss Institute of Bioinformatics

The Universal Protein Resource

http://www.uniprot.org/

Search in
Protein Knowledgebase (UniProtKB)
Query
Search Clear Fields »

Search | Blast | Align | Retrieve

WELCOME

The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

What we provide

UniProtKB	Protein knowledgebase, consists of two sections: Swiss-Prot, which is manually annotated and reviewed. TrEMBL, which is automatically annotated and is **not** reviewed.
UniRef	Sequence clusters, used to speed up similarity searches.
UniParc	Sequence archive, used to keep track of sequences and their identifiers.
Supporting data	Literature citations, taxonomy, keywords and more.

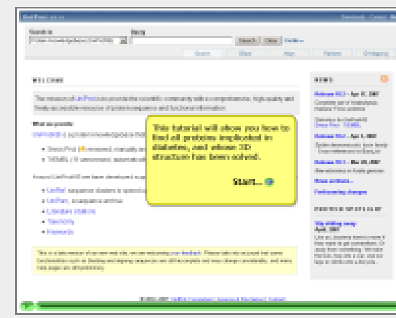
NEWS

Release 15.0 – Mar 24, 2009

Major release

- Statistics for UniProtKB: Swiss-Prot • TrEMBL
- Forthcoming changes
- News archives

SITE TOUR



Learn how to make best use of the tools and data on this site.

PROTEIN SPOTLIGHT

about the blues
March 2009

Every living being has devised a way to protect its embryos.

蛋白质结构数据库

- **PDB** 蛋白质数据仓库（Protein Data Bank）

  http://www.rcsb.org/pdb/

- **SCOP** 蛋白质结构分类数据库（ Structural classification of proteins ）

  http://scop.mrc-lmb.cam.ac.uk/scop/

蛋白质数据库

Expert **P**rotein **A**nalysis **Sy**stem

http://au.expasy.org/

Databases

- **UniProt Knowledgebase (Swiss-Prot and TrEMBL)** - Protein knowledgebase
- **ViralZone** - Portal to viral UniProtKB/Swiss-Prot entries new
- **PROSITE** - Protein families and domains
- **SWISS-2DPAGE** - Two-dimensional polyacrylamide gel electrophoresis
- **World-2DPAGE Repository** - A public standards-compliant repository for gel-based proteomics data published in the literature
- **MIAPEGelDB** - A public repository for MIAPE Gel electrophoresis documents
- **ENZYME** - Enzyme nomenclature
- **UniPathway** - Metabolic pathways
- **SWISS-MODEL Repository** - Automatically generated protein models

- Links to many other molecular biology databases

Tools and software packages

- **Proteomics and sequence analysis tools**
  - Identification and characterization (Aldente, FindMod, Popitam, Phenyx, pI/Mw, ProtParam...)
  - DNA -> Protein
  - Similarity searches (BLAST...)
  - Pattern and profile searches (ScanProsite...)
  - Post-translational modification and topology prediction
  - Primary structure analysis
  - Secondary and tertiary structure tools (Swiss-PdbViewer...)
  - Alignment and Phylogenetic analysis
- **Melanie / ImageMaster** - Software for 2-D PAGE analysis
- **MSight** - Mass Spectrometry Imager
- **Roche Applied Science's Biochemical Pathways**

Education and services

- **The ExPASy FTP server**
- **Swiss-Shop** - automatically obtain (by email) new sequence entries relevant to your field(s) of interest

- Popular Science
  - **Protein Spotlight**
  - **Protéines à la «Une»**

- **e-Proxemis** - Bioinformatics Learning Portal for Proteomics

- **Bioinformatics Core Facility for Proteomics**
- **Proteomics Core Facility** (formerly known as SWISS-2DSERVICE)

- **SPS' Digest** - the Swiss Proteomics Society selection of proteomics articles
- **Master's degree in Proteomics and Bioinformatics**

- **Swiss-Quiz**

Lists of molecular biology resources

- **ExPASy Life Science Directory** - The ExPASy list of biomolecular servers
- **BioHunt** - Search the internet for molecular biology information
- **WORLD-2DPAGE List** - Links to 2-D PAGE database servers and 2-D PAGE related servers and services
- **World-2DPAGE Portal** - A dynamic portal to query simultaneously World-Wide gel-based proteomics databases

Swiss Institute of Bioinformatics (SIB) services

- Vital-IT - The HPC Center for Life Sciences
- Swiss node of EMBnet

- Ashbya Genome Database
- Cancer Immunome Database

- CleanEx - Gene expression database
- EPD - Eukaryotic Promoter Database
- GermOnLine - Knowledgebase on germ cell differentiation
- smiRNAdb - a database of small RNAs
- SwissRegulon - a database of regulatory sites

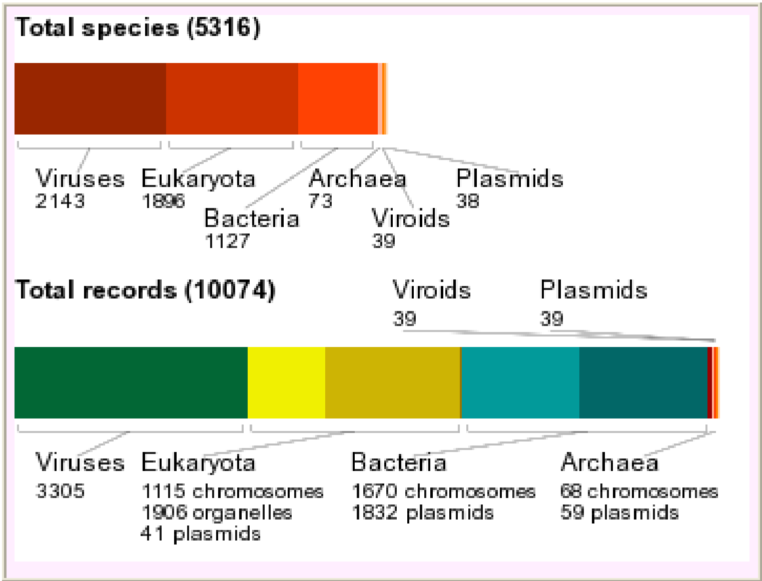
基因组学数据库

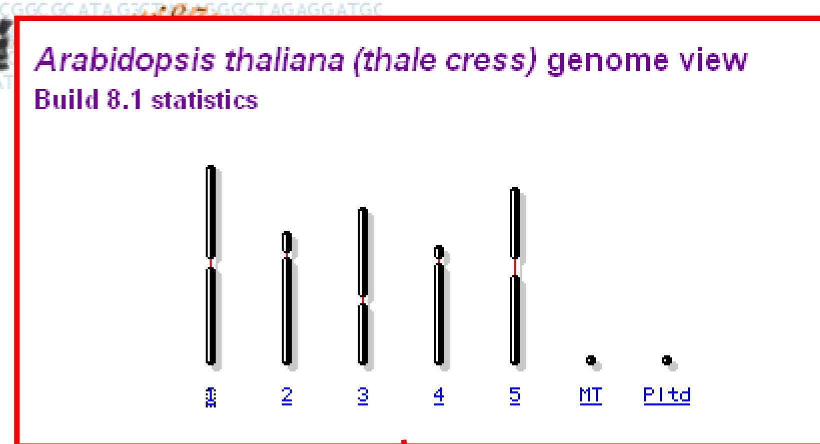
- 主要内容：基因组结构、基因单位、基因组图谱等（遗传图、叠连群图、放射杂交图等）
- 分布：由各国基因组研究中心组建，分布在世界各地的信息中心、研究机构。
- 代表性的基因组学数据库有：
  - 人类基因组数据库GDB

    http://www.gdb.org
  - 中国水稻基因组数据库

    http://www.csdb.cn/viewdb.jsp?uri=cn.csdb.ricegene
  - NCBI基因组数据库Genome

    http://www.ncbi.nlm.nih.gov





7
个，古生菌73个，类病毒39个，质粒38个

- 共收录基因组信息10074条
- 真核生物 Entrez Map View

Eukaryotae Complete Chromosomes Taxonomy / List Total: 1037

organism	name	accession	length	proteins	RNAs	genes	create_date	update_date
Arabidopsis thaliana	1	NC_003070	30432563 nt	8521	436	8337	Aug 13 2001	Aug 14 2008
Arabidopsis thaliana	2	NC_003071	19705359 nt	5182	225	5439	Jul 29 2002	Aug 14 2008
Arabidopsis thaliana	3	NC_003074	23470805 nt	6432	220	6680	Aug 13 2001	Aug 14 2008
Arabidopsis thaliana	4	NC_003075	18585042 nt	4935	180	5079	Aug 13 2001	Aug 14 2008
Arabidopsis thaliana	5	NC_003076	26992728 nt	7545	235	7468	Aug 13 2001	Aug 14 2008
Ashbya gossypii ATCC 10895	I	NC_005782	691920 nt	381	34	415	Mar 5 2004	Jun 11 2008

NCBI

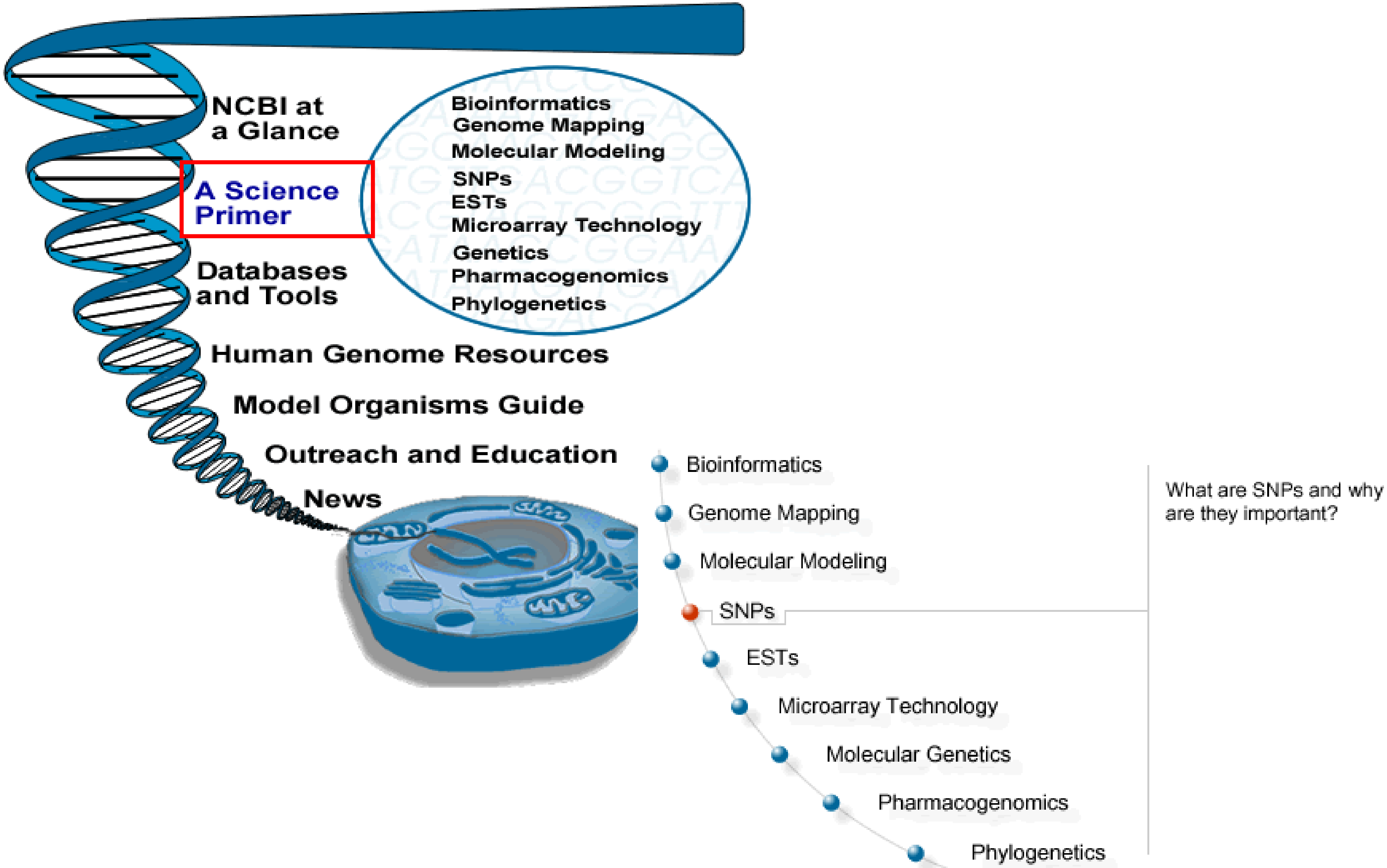
- 概述
- Entrez检索平台
- GenBank
- My NCBI
- Blast

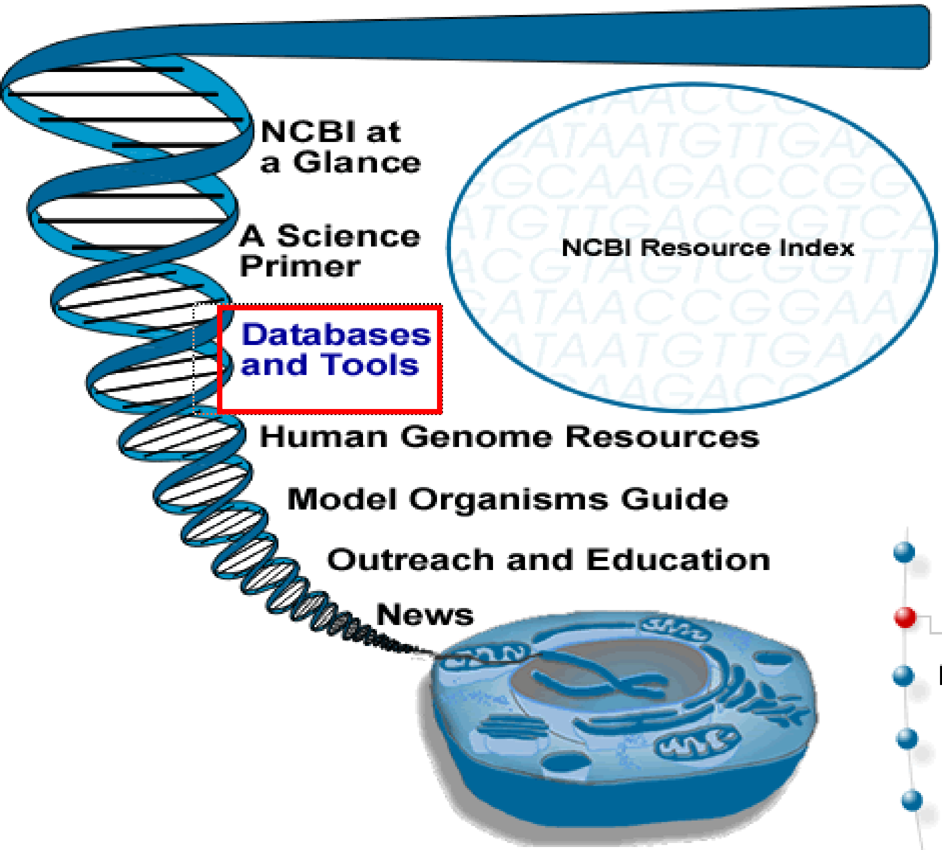
NCBI

National Center for Biotechnology Information

- NCBI是美国国立卫生研究院（NIH）的美国国立医学图书馆（NLM）的一个分支。
- 1988年 国立生物技术信息中心（NCBI）成立。
- **What does NCBI do?**

conducts research in computational biology, develops software tools for analyzing genome data, and disseminates biomedical information - all for the better understanding of molecular processes affecting human health and disease.

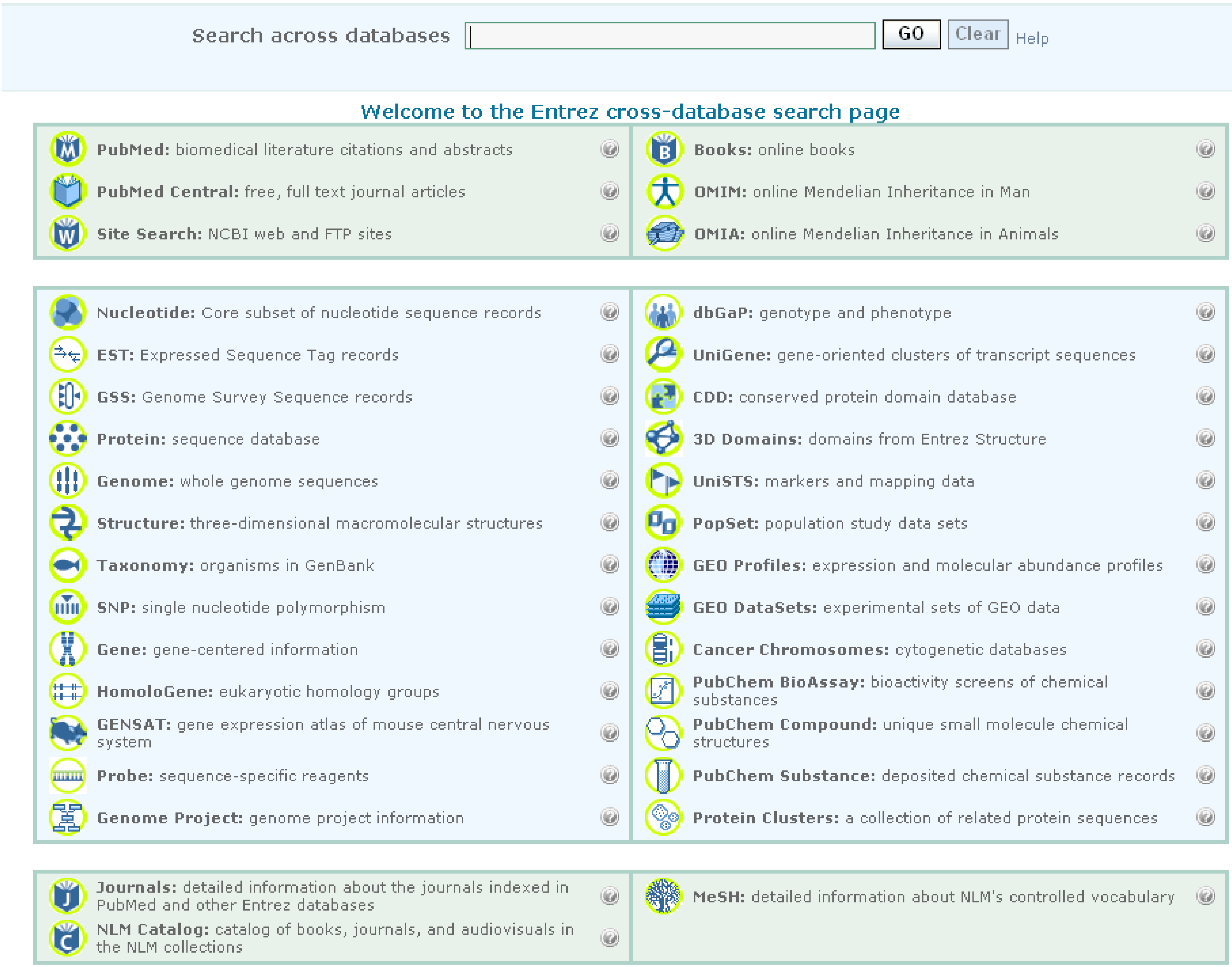

NCBI at a Glance
A Science Primer
Databases and Tools
Human Genome Resources
Model Organisms Guide
Outreach and Education
News
Bioinformatics
Genome Mapping
Molecular Modeling
SNPs
ESTs
Microarray Technology
Genetics
Pharmacogenomics
Phylogenetics
Bioinformatics
Genome Mapping
Molecular Modeling
SNPs
ESTs
Microarray Technology
Molecular Genetics
Pharmacogenomics
Phylogenetics
What are SNPs and why are they important?

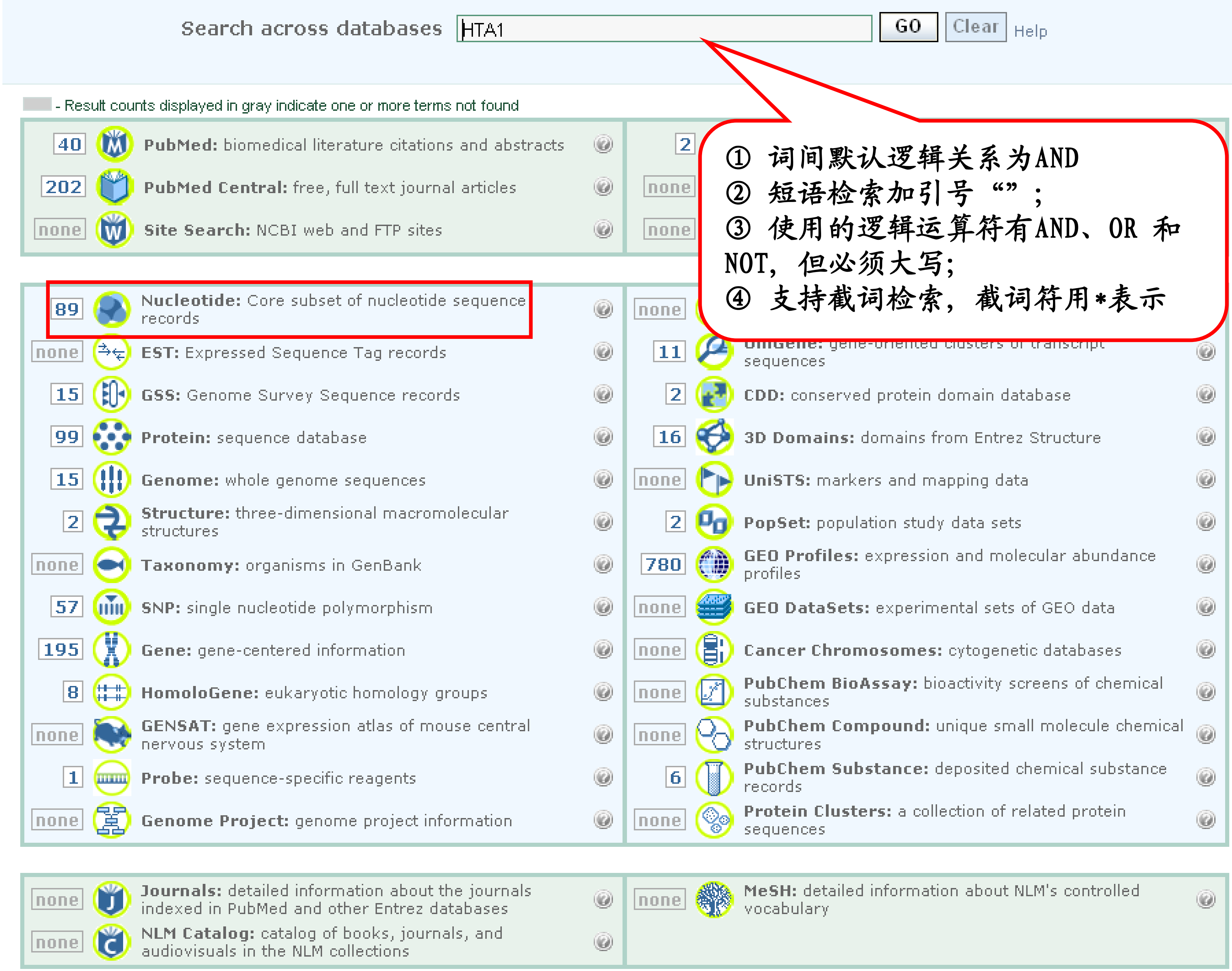


- Literature Databases
- Entrez Databases
- Nucleotide Databases
- Genome-Specific Resources
- Tools for Data Mining
- Tools for Sequence Analysis
- Tools for 3-D Structure Display and Similarity Searching
- Maps
- Collaborative Cancer Research
- FTP Download Sites
- Resource Statistics

Entrez is a retrieval system designed for searching several linked databases.

NCBI - Entrez 检索平台





① 词间默认逻辑关系为AND
② 短语检索加引号“”；
③ 使用的逻辑运算符有AND、OR 和 NOT，但必须大写；
④ 支持截词检索，截词符用*表示

GenBank



信息来源：
gb_GenBank
emb_EMBL
dbj_DDBJ
sp_SWISS-PROT
pdb_Protein Database
pir_PIR
prf_PRF
ref_RefSeq

Search Nucleotide for Go Clear

Limits Preview/Index History Clipboard Details

Format: **GenBank** FASTA Graphics More Formats Download Save Links

NCBI Reference Sequence: NM_124845.3

Arabidopsis thaliana HTA1/RAT5 (RESISTANT TO AGROBACTERIUM TRANSFORMATION 5); DNA binding (HTA1/RAT5)

Comment Features Sequence

```
LOCUS       NM_124845                669 bp    mRNA    linear   PLN 22-MAY-2008
DEFINITION  Arabidopsis thaliana HTA1/RAT5 (RESISTANT TO AGROBACTERIUM
            TRANSFORMATION 5); DNA binding (HTA1/RAT5) mRNA, complete cds.
ACCESSION   NM_124845
VERSION     NM_124845.3  GI:145359244
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta
            Spermatophyta; Magnoliophyta; eudicotyledons; core
            rosids; eurosids II; Brassicales; Brassicaceae; Ara
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
            NCBI review. The reference sequence was derived from AT5G54640.1.
            On Apr 18, 2007 this sequence version replaced gi:30696496.
FEATURES             Location/Qualifiers
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                     /chromosome="5"
                     /ecotype="Columbia"
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                     /gene_synonym="HTA1; MRB17.14; MRB17_14; RAT5; RESISTANT
                     TO AGROBACTERIUM TRANSFORMATION 5"
                     /function="Isolated from T-DNA insertion line, the rat5
                     mutant is deficient in T-DNA integration. Encodes
                     histone2A protein."
                     /db_xref="GeneID:835553"
                     /db_xref="TAIR:AT5G54640"
     CDS             64..456
```

座位号

物种来源

专业评论

特性

PLN子库: plant,fungal,algal

Change Region Shown

Customize View

Pick Primers

Design and test primers for this sequence Primer-BLAST.

Articles about HTA1/RAT5

Reference sequences

- Protein

More about the gene HTA1/RAT5

Also Known As: AT5G54640, HTA1, MRB

Homologs of HTA1/RAT5

The HTA1/RAT5 gene is conserved in dog rice, and P.falciparum.

Recent Activity

Turn Off

Arabidopsis thaliana HTA1/RAT5 (RESISTANT TO AGROBACTERI TRANSFORMATION 5); DNA bind

HTA1 Arabidopsis (12)

RecName: Full=Probable histone

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CDS             64..456
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                /locus_tag="AT5G54640"
                /gene_synonym="HTA1; MRB17.14; MRB17_14; RAT5; RESISTANT
                TO AGROBACTERIUM TRANSFORMATION 5"
                /note="Identical to Histone H2A.6 (RAT5) [Arabidopsis
                Thaliana] (GB:Q9LD28); similar to HTA13, DNA binding
                [Arabidopsis thaliana] (TAIR:AT3G20670.1); similar to HTA2
                (HISTONE H2A), DNA binding [Arabidopsis thaliana]
                (TAIR:AT4G27230.1); similar to HTA10, DNA binding
                [Arabidopsis thaliana] (TAIR:AT1G51060.1); similar to
                unnamed protein product [Vitis vinifera] (GB:CAO39058.1);
                similar to unknown [Populus trichocarpa] (GB:ABK94384.1);
                similar to unknown [Populus trichocarpa] (GB:ABK94182.1);
                contains InterPro domain Histone-fold;
                (InterPro:IPR009072); contains InterPro domain Histone
                core; (InterPro:IPR007125); contains InterPro domain
                Histone H2A; (InterPro:IPR002119)"
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                /product="HTA1/RAT5 (RESISTANT TO AGROBACTERIUM
                TRANSFORMATION 5); DNA binding"
                /protein_id="NP_200275.1"
                /db_xref="GI:15239697"
                /db_xref="GeneID:835553"
                /db_xref="TAIR:AT5G54640"
                /translation="MAGRGKTLGSGGAKKATSRSSKAGLQFPVGRIARFLKAGKYAER
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ORIGIN
        1 gttaatttcg tcaagaaaaa aattcgattt ttttgcgctc tttgtgggtt gttgttgttg
       61 aaaatggctg gtcgtggaaa aactcttgga tccggtgggg cgaagaaagc tacatctcgg
      121 agtagcaaag ccggtcttca attcccggtg ggtcgtatcg ctcgtttctt aaaagccggt
      181 aaatacgccg aacgtgttgg tgccggtgct ccggtttatc tcgccgccgt tctcgaatat
      241 ttggccgccg aggttcttga attagctgga aacgcagcaa gagacaacaa gaagacacgt
      301 attgttcc                                acgatg aggagctaag caagcttctt
      361 ggagatgt                                ctaaca tccacaatct ccttctccct
      421 aagaaggc                                aggtct tttaacacaa tgatatagaa
      481 cacgtctctc ttttggcttt agatctaata acctaataac tagctagatg ttttcacttt
      541 ttgtatcttt gcttttttta attcctttag ggatttgttt ctttccgttt ctgtttcgac
      601 atgttgtttc tgtttttgtg aatatatgaa agtattttgc gaaatatgaa tgataatgtc
      661 tttcaaaaa
//
```

RecName: Full=Probable his

LOC_Os01g31800 (1)

Os01g31800 (0)

All links from this record

- Gene
- Genome
- Genome Project
- ome Project
- oloGene
- Probe
- Protein
- PubMed (RefSeq)
- bMed (Weighted)
- xonomy
- Related Sequences
- Map Viewer
- GEO Profiles
- UniGene
- LinkOut

蛋白质序列

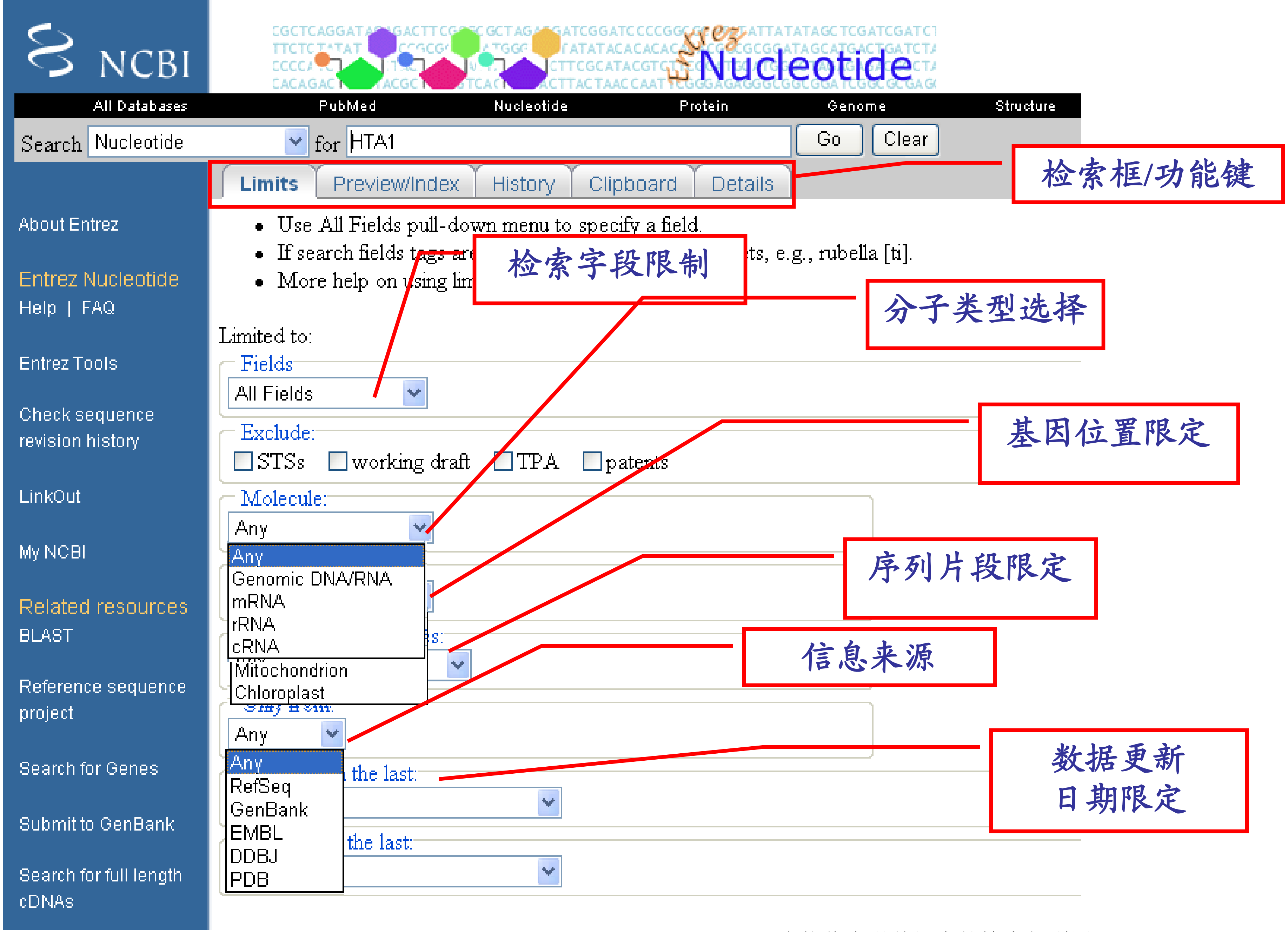
碱基序列

序列开始标志

序列终止标志

GenBank的主要字段及其含义

字段	含义	解释
LOCUS	Identifier	序列名称、性质描述
ACCESSION	Accession number	序列接受号
DEFINITION	Description	序列定义
KEYWORDS	Keywords	关键词
SOURCE	Organism(species)	来源种属
ORGANISM	Organism(classification)	来源分类
REFERENCE	Reference number	参文条目
AUTHORS	Reference authors	参文作者
TITLE	Reference title	参文题目
JOURNAL	Reference location	参文出处
COMMENTS	Database cross-reference	交叉索引
MEDLINE	Medline number	MEDLINE号
FEATURES	Feature table header data	序列性质表头数据
BASE COUNT		碱基数目
ORIGIN		序列开始标志
//	Termination line	序列终止标志


NCBI
Entrez Nucleotide
All Databases
PubMed
Nucleotide
Protein
Genome
Structure
Search
Nucleotide
for
HTA1
Go
Clear
Limits
Preview/Index
History
Clipboard
Details
检索框/功能键
Use All Fields pull-down menu to specify a field.
If search fields tags are
ts, e.g., rubella [ti].
More help on using lim
检索字段限制
分子类型选择
Limited to:
Fields
All Fields
基因位置限定
Exclude:
STSs
working draft
TPA
patents
Molecule:
Any
Any
Genomic DNA/RNA
mRNA
rRNA
cRNA
Mitochondrion
Chloroplast
序列片段限定
信息来源
Any
Any
RefSeq
GenBank
EMBL
DDBJ
PDB
the last:
the last:
数据更新
日期限定
About Entrez
Entrez Nucleotide
Help | FAQ
Entrez Tools
Check sequence revision history
LinkOut
My NCBI
Related resources
BLAST
Reference sequence project
Search for Genes
Submit to GenBank
Search for full length cDNAs

提供用户预览检索结果和索引检索、修改检索式的方便

Limits | **Preview/Index** | History | Clipboard | Details

- Enter terms and click Preview to see only the number of search results.
- To save search indefinitely, click query # and select Save in My NCBI.
- To combine searches use #search, e.g., #2 AND #3 or click query # for more options.

Search	Most Recent Queries	Time	Result
#37	Select 1 document(s)	01:36:55	1
#9	Search **HTA1 Arabidopsis**	01:29:07	12
#29	Search **Os01g31800**	01:24:06	0

Add Term(s) to Query or View Index:

- Enter a term in the text box; use the pull-down menu to specify a search field.
- Click Preview to add terms to the query box and see the number of search results, or click Index to view terms within a field.

All Fields [ ] Preview Index

Click AND OR NOT to add a term to the query box

NCBI

Entrez PubMed Nucleotide Protein Genome Structure OMIM PMC

Advanced Entrez Tools

Web Tools:

Batch Entrez - Upload a file of GI or accession numbers to retrieve sequences.

PubMed Batch Citation Matcher - Send citation information to Entrez and retrieve PubMed IDs for linking, citation display, or other applications.

Advanced Entrez Searching - Advanced searching techniques for Web Entrez.

My NCBI - includes automatic e-mailing of search updates and filters for search results.

Programming Tools:

E-Utilities - Run Entrez queries and download data from your own scripts over the Web.

Linking to Entrez - Link to specific Entrez pages from your own web pages or applications.

Entrez Client/Server - C language library for embedding Entrez calls into your programs.

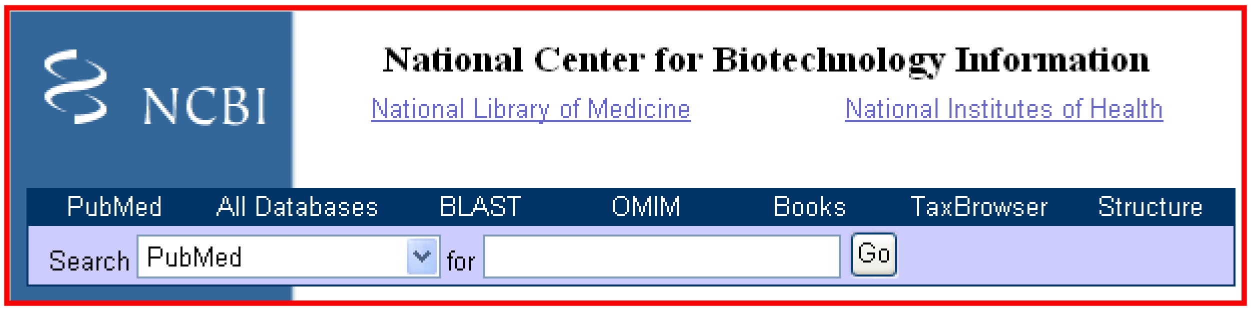
My NCBI

- What Is My NCBI?
- Getting Started
- Saving and Managing Searches
- Collections
- My Bibliography
- Using Preferences
- Working with Filters
- Using My NCBI to Set Up LinkOut
- Other Resources at My NCBI
- Tutorials

(Saving and Managing Searches, Collections, My Bibliography:) **My Saved Data**

My NCBI - What Is My NCBI & Getting Started

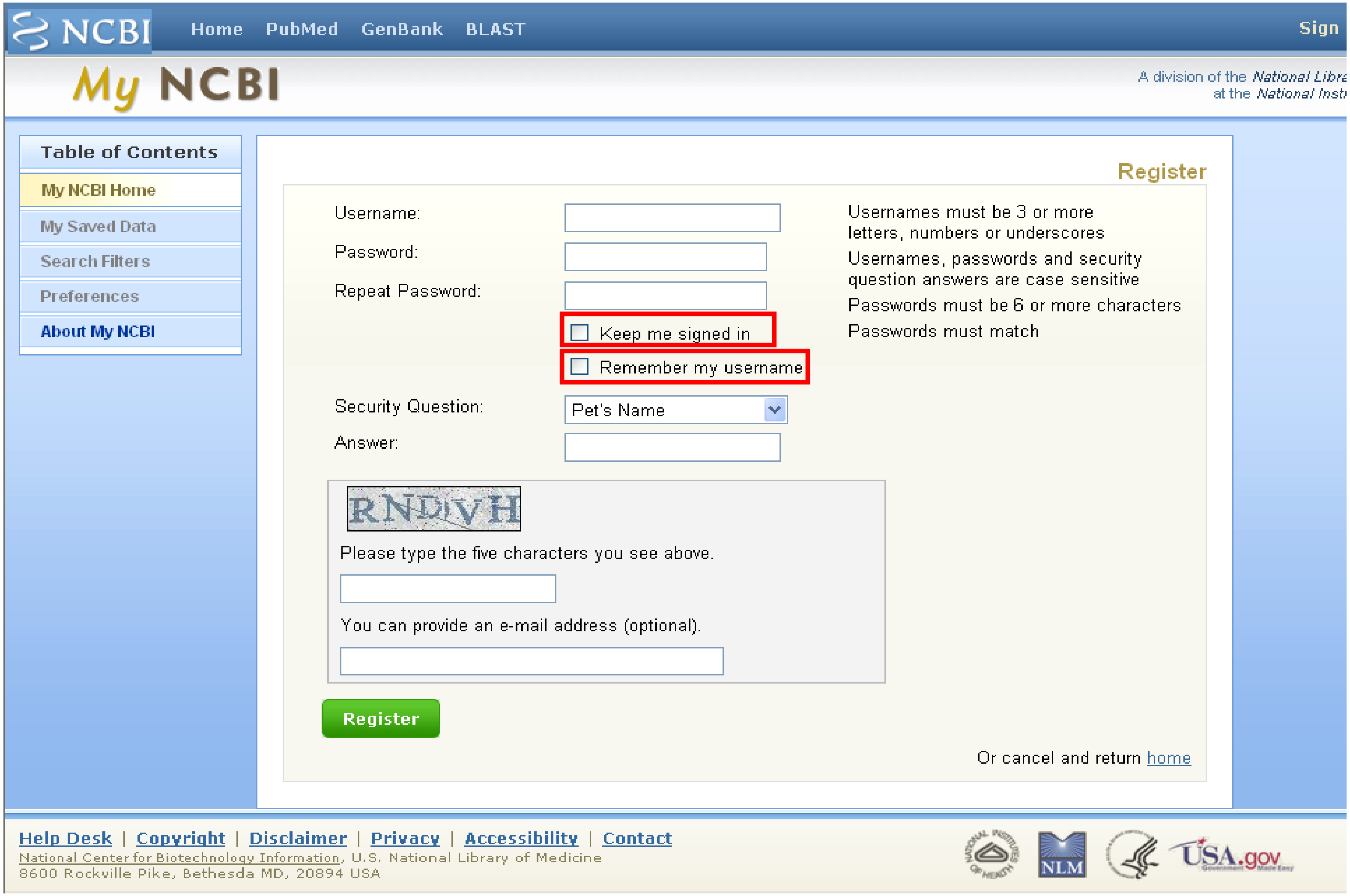
- A tool that retains user information and preferences to provide customized services. It allows you to save searches, select filtering options, and set up automatic searches that are sent by e-mail.
- Set up a My NCBI account





Hot Spots

- Clusters of orthologous groups
- Coffee Break, Genes & Disease, NCBI Handbook
- Electronic PCR
- Entrez Home
- Entrez Tools
- Gene expression omnibus (GEO)
- Human genome resources
- Influenza Virus Resource
- Map Viewer
- dbMHC
- Mouse genome resources
- My NCBI
- ORF finder
- Rat genome resources


NCBI
Home PubMed GenBank BLAST
Sign
My NCBI
A division of the National Libra
at the National Insti
Table of Contents
My NCBI Home
My Saved Data
Search Filters
Preferences
About My NCBI
Register
Username:
Password:
Repeat Password:
Keep me signed in
Remember my username
Security Question:
Pet's Name
Answer:
Usernames must be 3 or more letters, numbers or underscores
Usernames, passwords and security question answers are case sensitive
Passwords must be 6 or more characters
Passwords must match
RNDVH
Please type the five characters you see above.
You can provide an e-mail address (optional).
Register
Or cancel and return home
Help Desk | Copyright | Disclaimer | Privacy | Accessibility | Contact
National Center for Biotechnology Information, U.S. National Library of Medicine
8600 Rockville Pike, Bethesda MD, 20894 USA
NLM
USA.gov


My NCBI
Welcome xiaoweihe. [Sign Out]

My NCBI — Saving and Managing Searches

- Saving a Search in My NCBI
- Setting Up Automatic E-mail Updates
- Running Saved Searches and Checking for New Results
- Sorting Searches
- Deleting a Search

Saving a Search in My NCBI



Setting Up Automatic E-mail Updates

- ✓ Validate – 要先确认邮箱

Note: Your My NCBI account will *not* send email to any email address that has not been validated. This means that automatic updates for saved searches will not be emailed. So, it is important to watch for this email and respond to it.

Table of Contents

My NCBI Home

My Saved Data

Search Filters

Preferences

About My NCBI

Saved Search Settings

Your Nucleotide search

Search: HTA

Name of Search: HTA

E-mail:

Your email address, xiaoweihe@zjuem.zju.edu.cn, hasn't been validated yet. To receive search e-mails please...

Click save on the e-mail preferences page to send a confirmation e-mail to that address.

Click the confirmation link in the e-mail.

If you don't receive a confirmation e-mail, you should check your SPAM filtering software.

Would you like e-mail updates of new search results?

- (•) No thanks.
- ( ) Yes, once a month.
  Which day? the first Saturday
- ( ) Yes, once a week.
  Which day? Saturday
- ( ) Yes, every day.

Formats:

- (•) Send HTML e-mail
- ( ) Send text e-mail

Report format: Summary

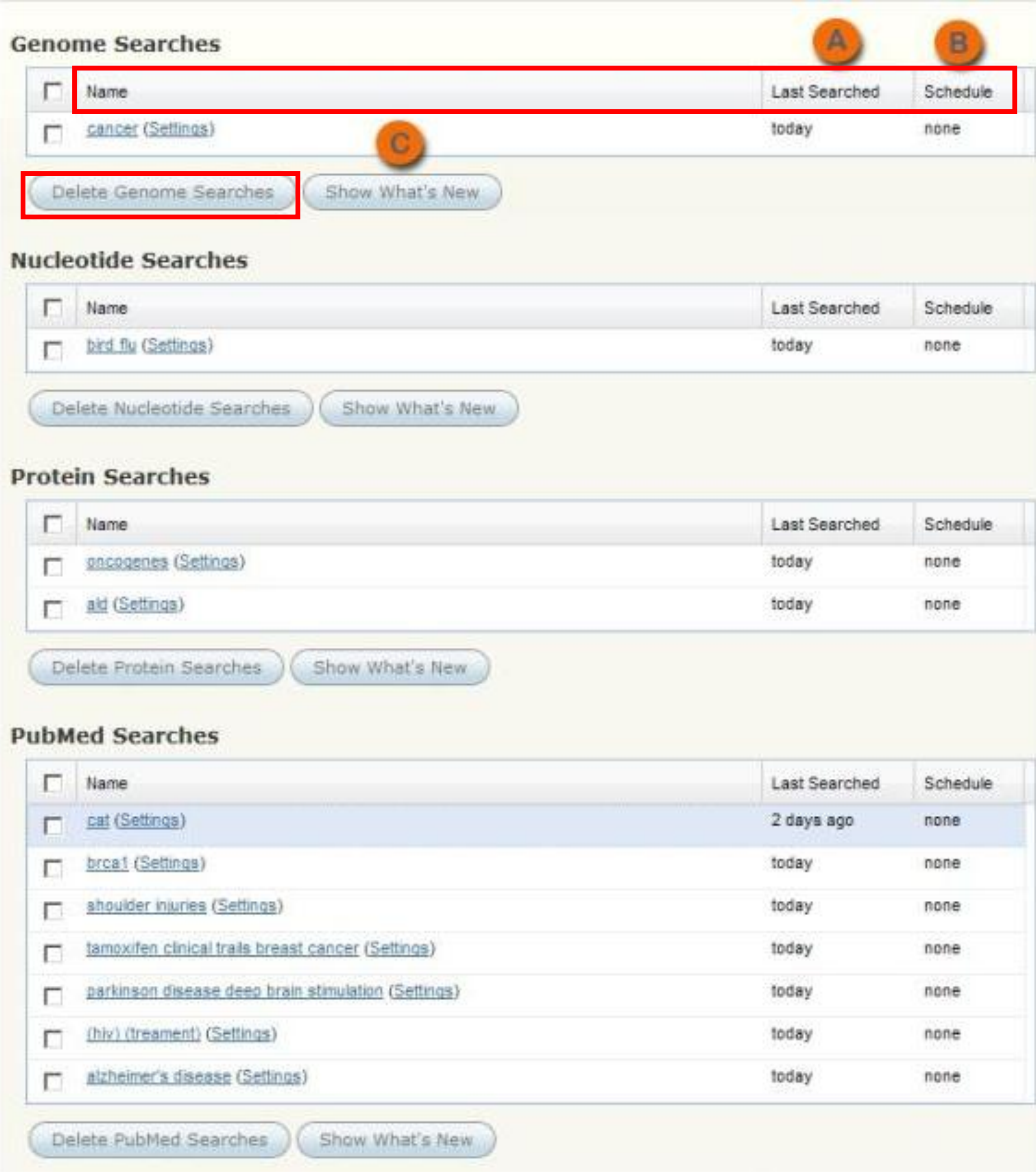
Number of items:

Send at most: 5 items ☐ Send even when there aren't any new results

Any text you want to be added at the top of your e-mail (optional):

Save

Or cancel and return to your search, or your Saved Searches



- Running Saved Searches and Checking for New Results
- Sorting Searches
- Deleting a Search

My NCBI — Using Preferences



NCBI

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Items 1 - 20 of 2255672 Page 1 of 112784 Next

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Help | FAQ
Tutorials
New/Noteworthy
E-Utilities

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MeSH Database
Single Citation Matcher
Batch Citation Matcher
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Special Queries
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1: Zhejiang Da Xue Xue Bao Yi Xue Ban. 2009 Mar;38(2):208-14. Related Articles

[Function of TM4SF-integrins complexes in regulating cancer metastasis.]

[Article in Chinese]

Zhu LJ, Lai C.

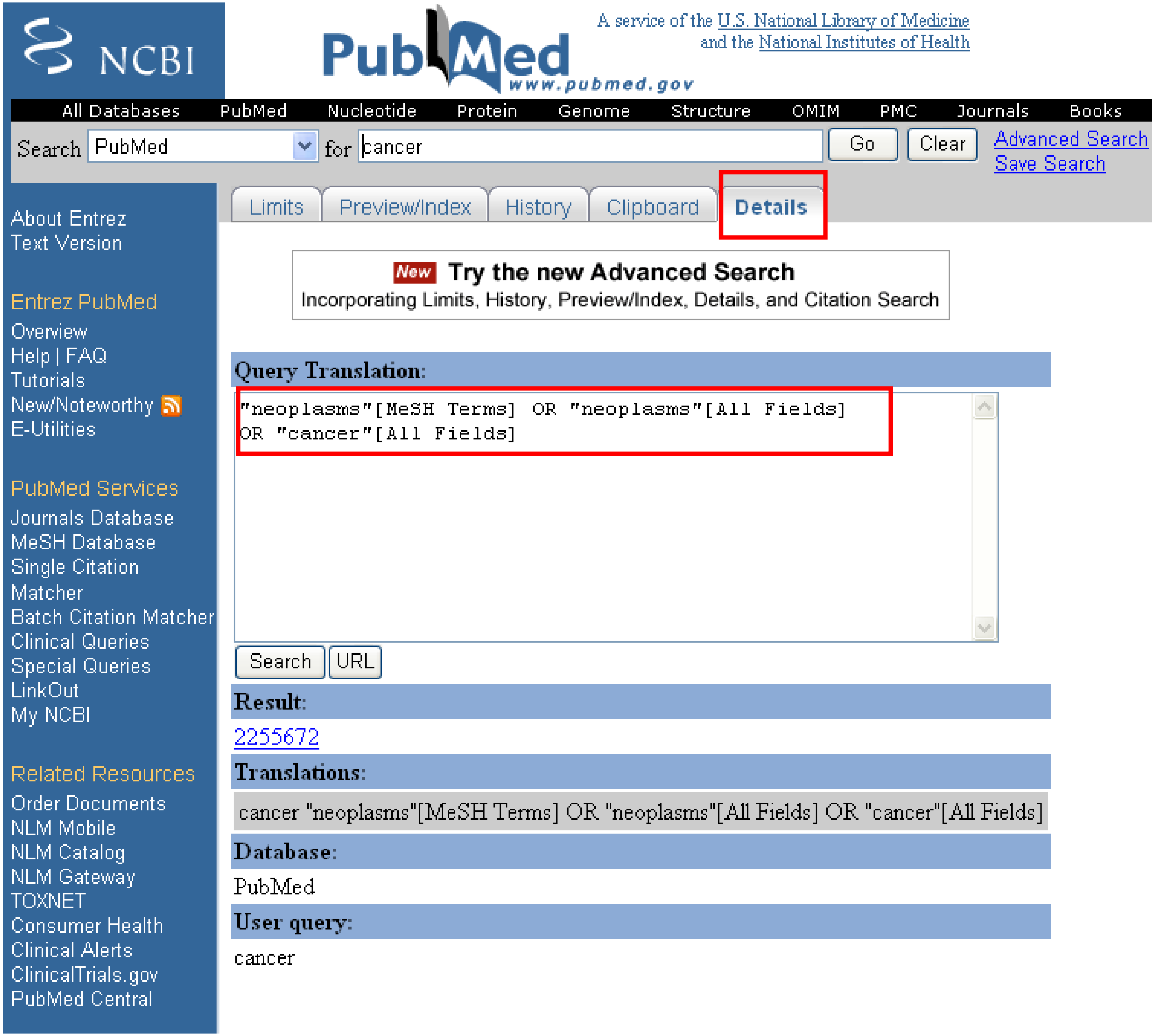
Laboratory for Thrombosis and Haemostasis Research, Department of Pathology, College of Medicine, Zhejiang University, Hangzhou 310058, China.

Distant metastasis is the main cause of cancer death. Tetraspanins (transmembrane 4 superfamily, TM4SF) is capable of forming transmembrane complexes with integrin family participating in cell adhesion, migration and tumor metastasis. This review elucidates the structure of tetraspanins and its function in regulating metastasis as form of multimolecular transmembrane complexes with integrin.

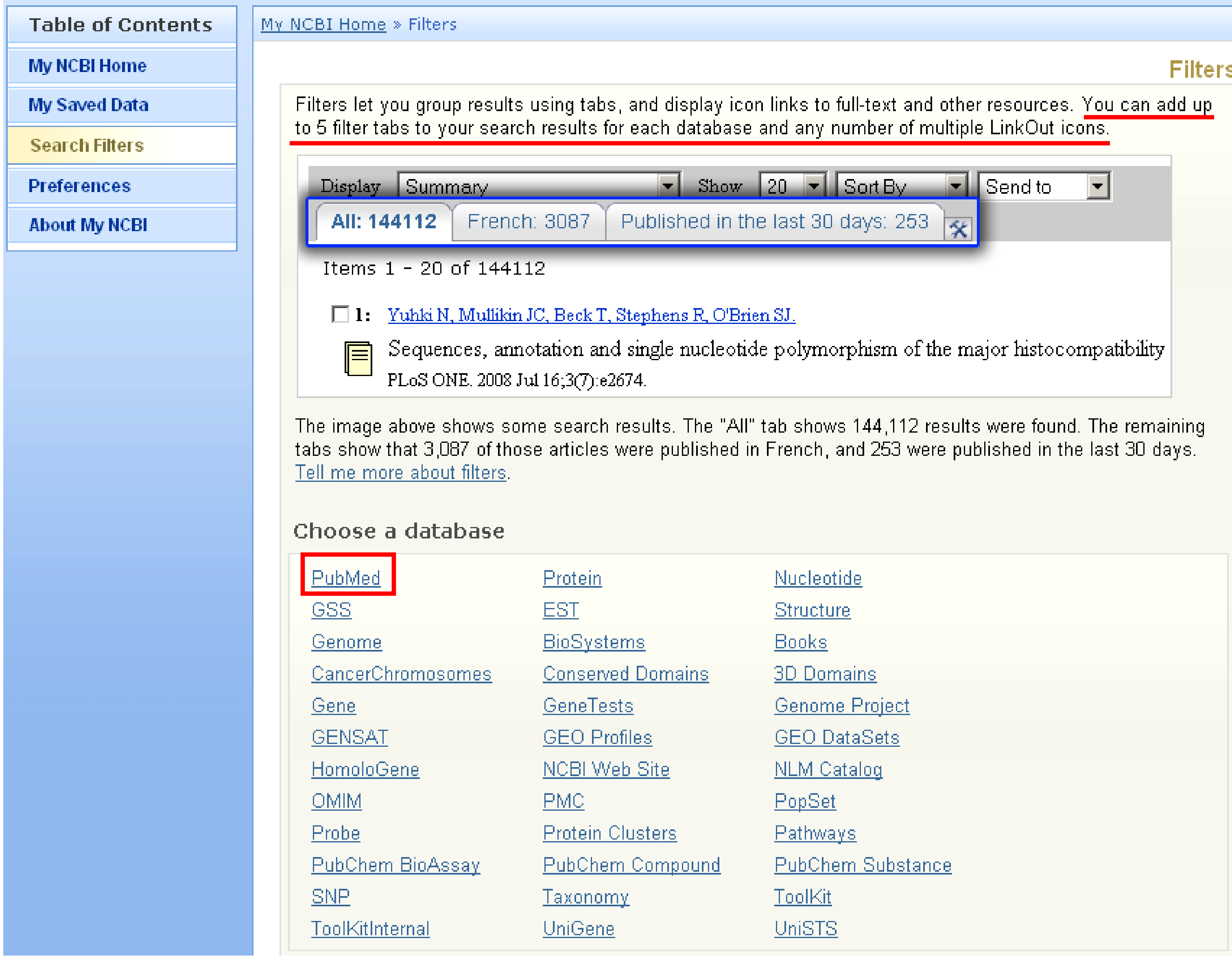
Publication Types:
- English Abstract

PMID: 19363832 [PubMed - in process]

2: Zhejiang Da Xue Xue Bao Yi Xue Ban. 2009 Mar;38(2):194-8. Related Articles


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New Try the new Advanced Search
Incorporating Limits, History, Preview/Index, Details, and Citation Search
Query Translation:
"neoplasms"[MeSH Terms] OR "neoplasms"[All Fields] OR "cancer"[All Fields]
Search URL
Result:
2255672
Translations:
cancer "neoplasms"[MeSH Terms] OR "neoplasms"[All Fields] OR "cancer"[All Fields]
Database:
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cancer

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Table of Contents

- My NCBI Home
- My Saved Data
- Search Filters
- Preferences
- About My NCBI

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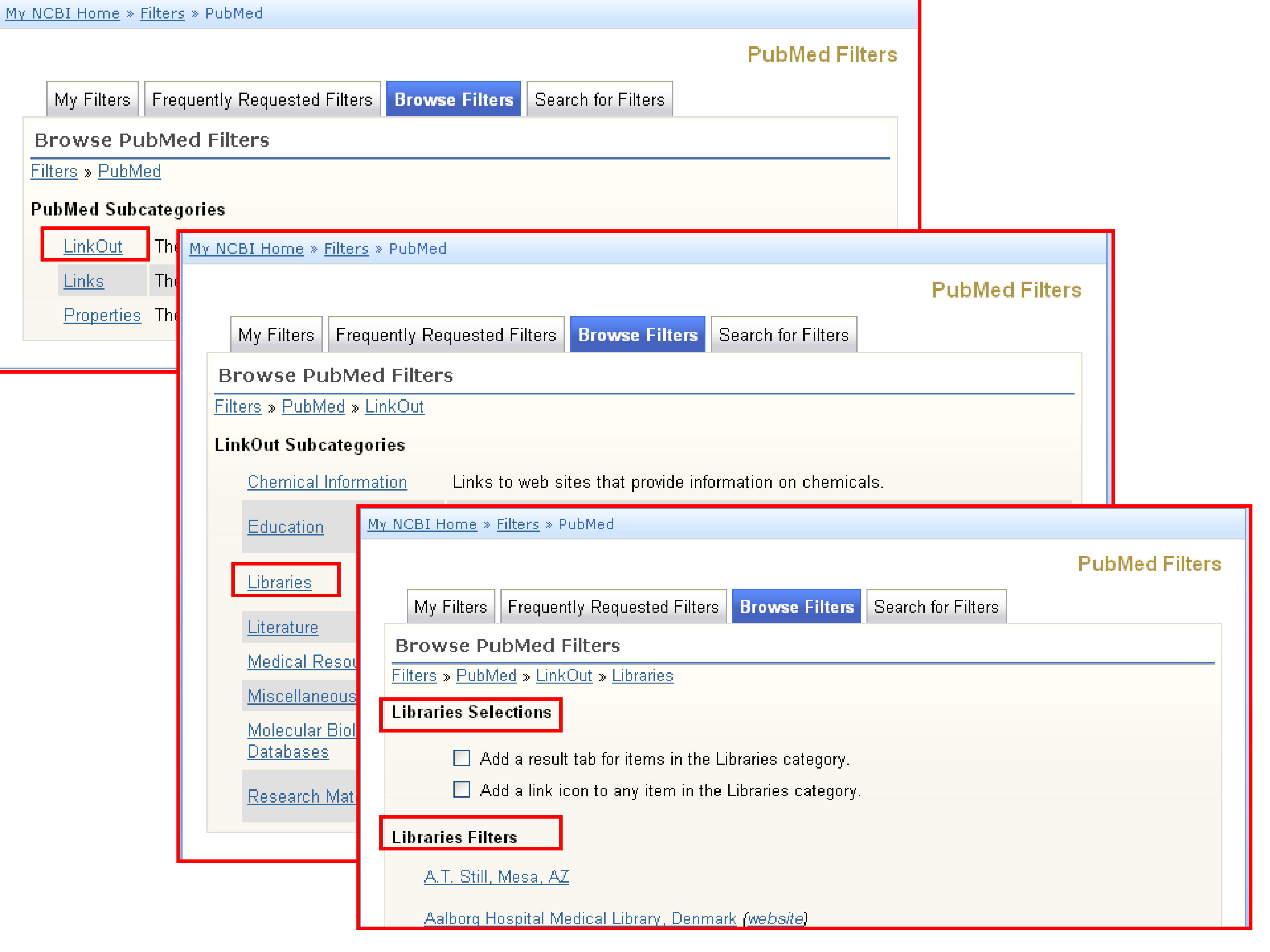
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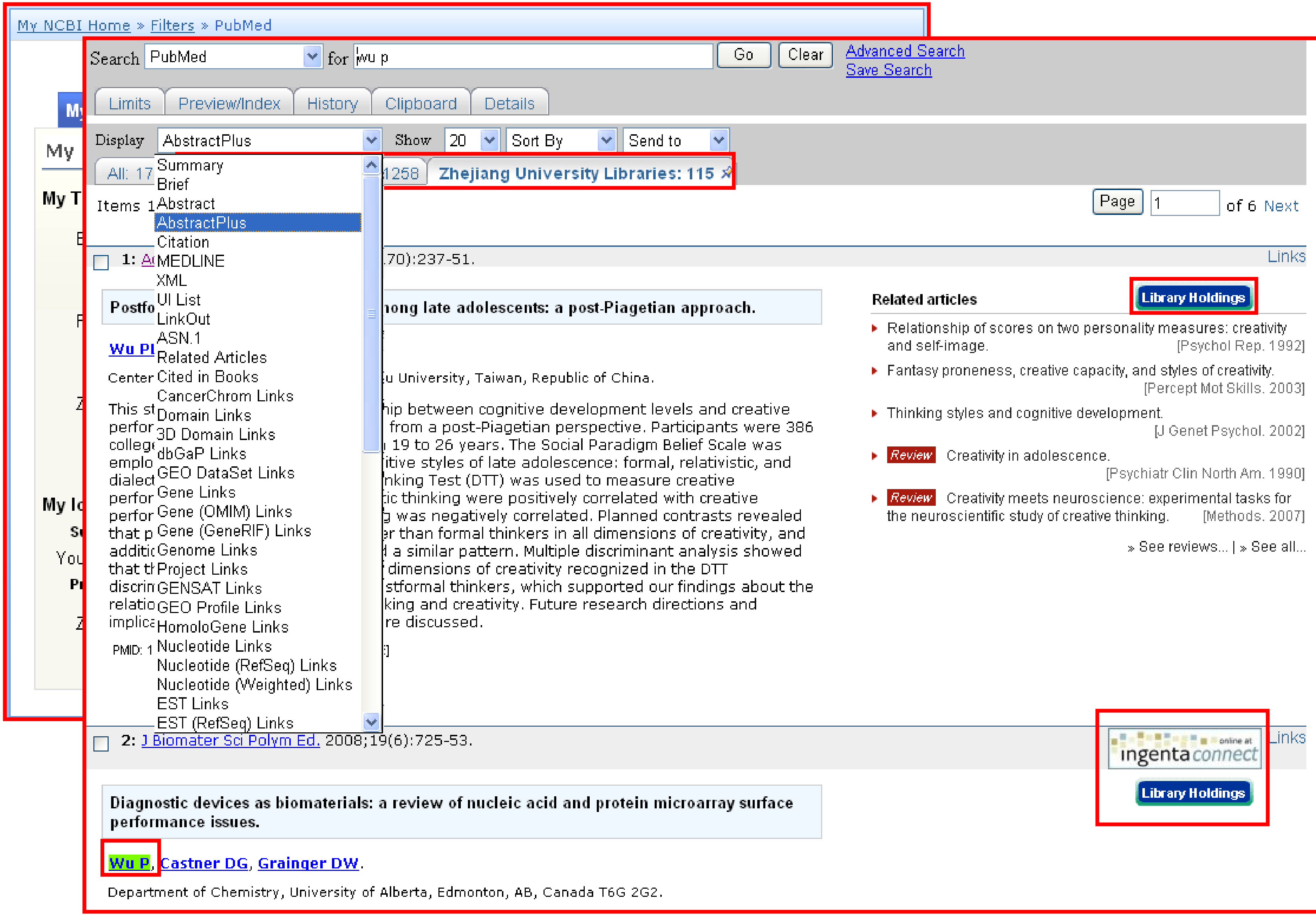
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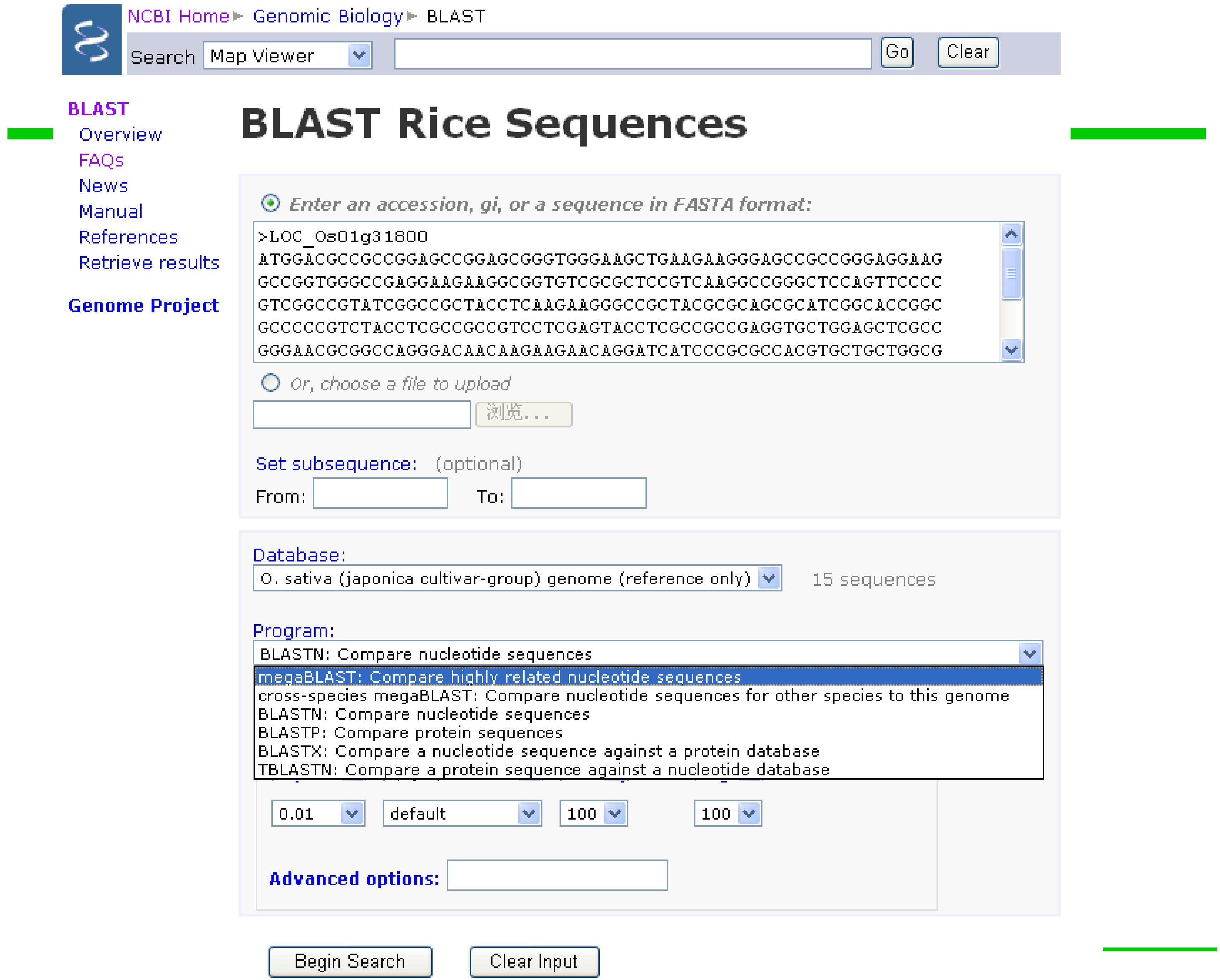

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Aalborg Hospital Medical Library, Denmark (website)

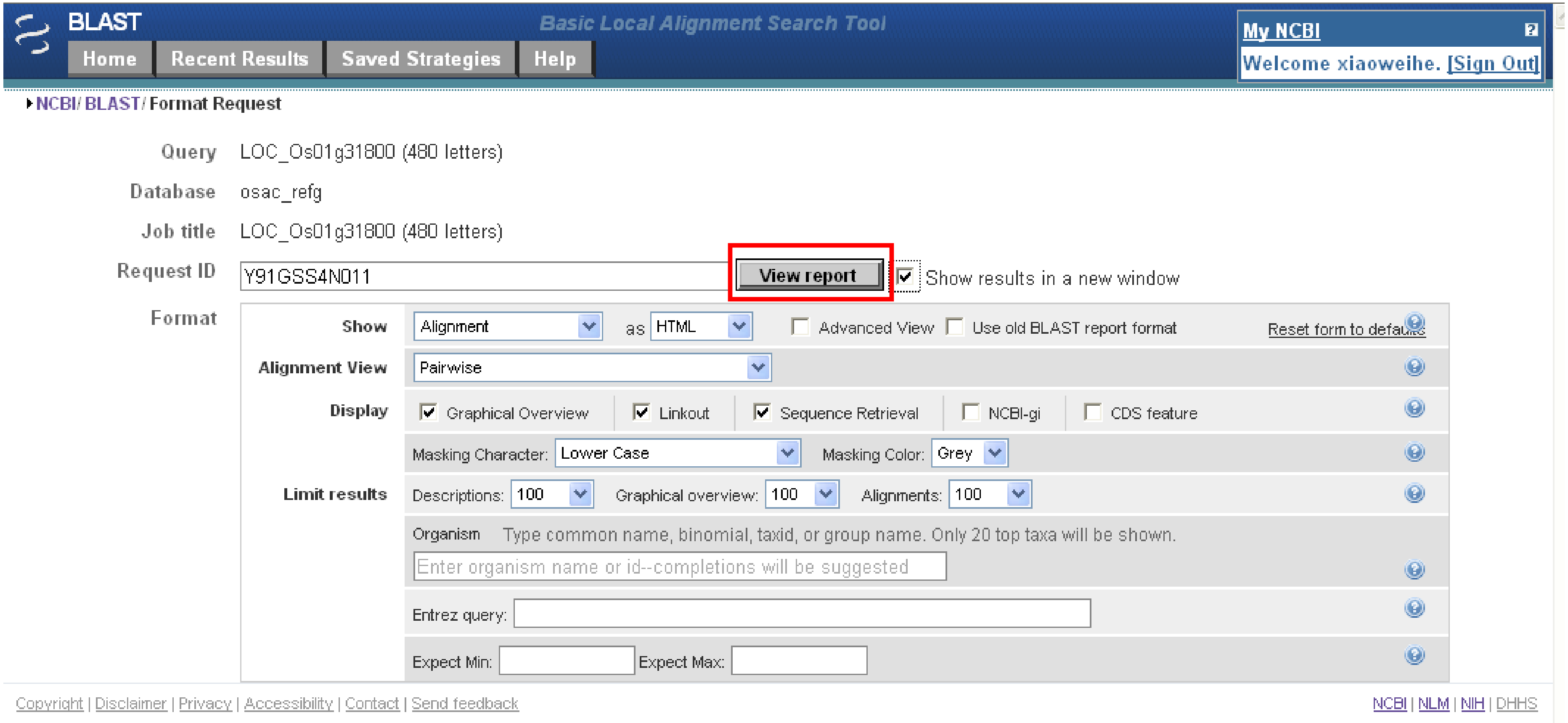

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Page 1 of 6 Next
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Fantasy proneness, creative capacity, and styles of creativity. [Percept Mot Skills. 2003]
Thinking styles and cognitive development. [J Genet Psychol. 2002]
Review Creativity in adolescence. [Psychiatr Clin North Am. 1990]
Review Creativity meets neuroscience: experimental tasks for the neuroscientific study of creative thinking. [Methods. 2007]
» See reviews... | » See all...
2: J Biomater Sci Polym Ed. 2008;19(6):725-53.
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Diagnostic devices as biomaterials: a review of nucleic acid and protein microarray surface performance issues.
Wu P, Castner DG, Grainger DW.
Department of Chemistry, University of Alberta, Edmonton, AB, Canada T6G 2G2.

Blast- Basic Local Alignment Search Tool



- BLAST Assembled Genomes
- Basic BLAST
- Specialized BLAST


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Search
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References
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Genome Project
BLAST Rice Sequences
Enter an accession, gi, or a sequence in FASTA format:
>LOC_Os01g31800
ATGGACGCCGCCGGAGCCGGAGCGGGTGGGAAGCTGAAGAAGGGAGCCGCCGGGAGGAAG
GCCGGTGGGCCGAGGAAGAAGGCGGTGTCGCGCTCCGTCAAGGCCGGGCTCCAGTTCCCC
GTCGGCCGTATCGGCCGCTACCTCAAGAAGGGCCGCTACGCGCAGCGCATCGGCACCGGC
GCCCCCGTCTACCTCGCCGCCGTCCTCGAGTACCTCGCCGCCGAGGTGCTGGAGCTCGCC
GGGAACGCGGCCAGGGACAACAAGAAGAACAGGATCATCCCGCGCCACGTGCTGCTGGCG
Or, choose a file to upload
浏览...
Set subsequence: (optional)
From:
To:
Database:
O. sativa (japonica cultivar-group) genome (reference only)
15 sequences
Program:
BLASTN: Compare nucleotide sequences
megaBLAST: Compare highly related nucleotide sequences
cross-species megaBLAST: Compare nucleotide sequences for other species to this genome
BLASTN: Compare nucleotide sequences
BLASTP: Compare protein sequences
BLASTX: Compare a nucleotide sequence against a protein database
TBLASTN: Compare a protein sequence against a nucleotide database
0.01
default
100
100
Advanced options:
Begin Search
Clear Input



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Help
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Query
LOC_Os01g31800 (480 letters)
Database
osac_refg
Job title
LOC_Os01g31800 (480 letters)
Request ID
Y91GSS4N011
View report
Show results in a new window
Format
Show
Alignment
as
HTML
Advanced View
Use old BLAST report format
Reset form to defaults
Alignment View
Pairwise
Display
Graphical Overview
Linkout
Sequence Retrieval
NCBI-gi
CDS feature
Masking Character:
Lower Case
Masking Color:
Grey
Limit results
Descriptions:
100
Graphical overview:
100
Alignments:
100
Organism
Type common name, binomial, taxid, or group name. Only 20 top taxa will be shown.
Enter organism name or id--completions will be suggested
Entrez query:
Expect Min:
Expect Max:
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LOC_Os01g31800 (480 letters)

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Alignment	Search Strategies	Bioseq
Text XML ASN.1 Hit Table(text) Hit Table(csv)	ASN.1	ASN.1

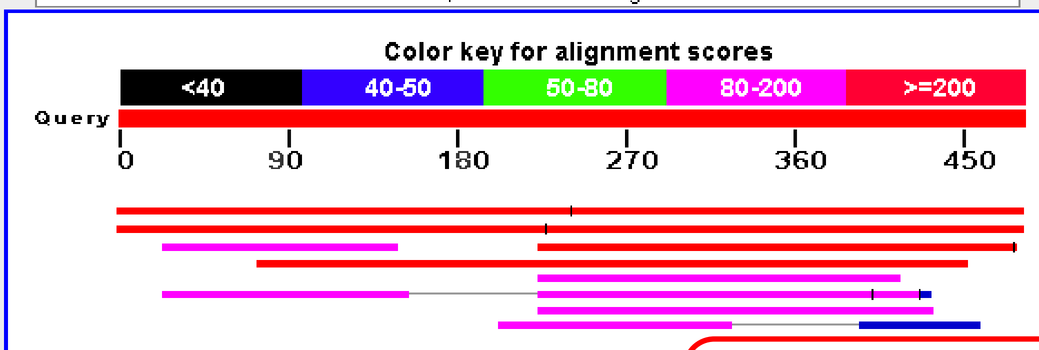
Query ID	lcl|879	**Database Name**	gp/39947.9512/osac_refg
Description	LOC_Os01g31800	**Description**	Oryza sativa Japonica Group O. sativa (japonica cultivar-group) genome (reference only)
Molecule type	nucleic acid		
Query Length	480	**Program**	BLASTN 2.2.20+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Japanese rice genome view]

Graphic Summary

Distribution of 23 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments



Bit分值：分值越高，比对越好

Descriptions

E值：序列比对的统计学显著性指标。E值越低，则比对就更有可能具有显著性。

Sequences producing significant alignments:		Score (Bits)	E Value
ref|NC_008394.1|	Oryza sativa (japonica cultivar-group) genom...	464	2e-129
ref|NC_008396.1|	Oryza sativa (japonica cultivar-group) genom...	455	1e-126
ref|NC_008398.1|	Oryza sativa (japonica cultivar-group) genom...	295	2e-78
ref|NC_008397.1|	Oryza sativa (japonica cultivar-group) genom...	230	8e-59

Alignments Select All Get selected sequences Distance tree of results

```
>ref|NC_008394.1| D Oryza sativa (japonica cultivar-group) genomic DNA, chromosome
1
Length=43261740

 Features in this part of subject sequence:
   hypothetical protein


 Score =  464 bits (514),  Expect = 2e-129
 Identities = 257/257 (100%), Gaps = 0/257 (0%)
 Strand=Plus/Plus

Query  224       aggtgctggagctcgccgggaacgcggccAGGGACAACAAGAAGAACAGGATCATCCCGC  283
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17416974  AGGTGCTGGAGCTCGCCGGGAACGCGGCCAGGGACAACAAGAAGAACAGGATCATCCCGC  17417033

Query  284       GCCACGTGCTGCTGGCGATCAGGAACGACGAGGAGCTCGGCAAGCTGCTGGCCGGCGTGA  343
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17417034  GCCACGTGCTGCTGGCGATCAGGAACGACGAGGAGCTCGGCAAGCTGCTGGCCGGCGTGA  17417093

Query  344       CCATCGCGCACGGAGGCGTGCTGCCCAACATCAACCCGGTGCTGCTGCCCAAGAAGACGG  403
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17417094  CCATCGCGCACGGAGGCGTGCTGCCCAACATCAACCCGGTGCTGCTGCCCAAGAAGACGG  17417153

Query  404       CGGAGAAGGCCGCCGCCGCCGGCAAGGAGGCCAAGTCGCCCAAGAAGGCGGCCGGCAAGT  463
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17417154  CGGAGAAGGCCGCCGCCGCCGGCAAGGAGGCCAAGTCGCCCAAGAAGGCGGCCGGCAAGT  17417213

Query  464       CCCCCAAGAAGGCCTAG  480
                 |||||||||||||||||
Sbjct  17417214  CCCCCAAGAAGGCCTAG  17417230


 Features in this part of subject sequence:
   hypothetical protein


 Score =  410 bits (454),  Expect = 4e-113
 Identities = 235/240 (97%), Gaps = 0/240 (0%)
 Strand=Plus/Plus
```

Blast- Basic BLAST

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a **nucleotide** database using a **nucleotide** query *Algorithms:* blastn, megablast, discontiguous megablast
protein blast	Search **protein** database using a **protein** query *Algorithms:* blastp, psi-blast, phi-blast
blastx	Search **protein** database using a **translated nucleotide** query
tblastn	Search **translated nucleotide** database using a **protein** query
tblastx	Search **translated nucleotide** database using a **translated nucleotide** query

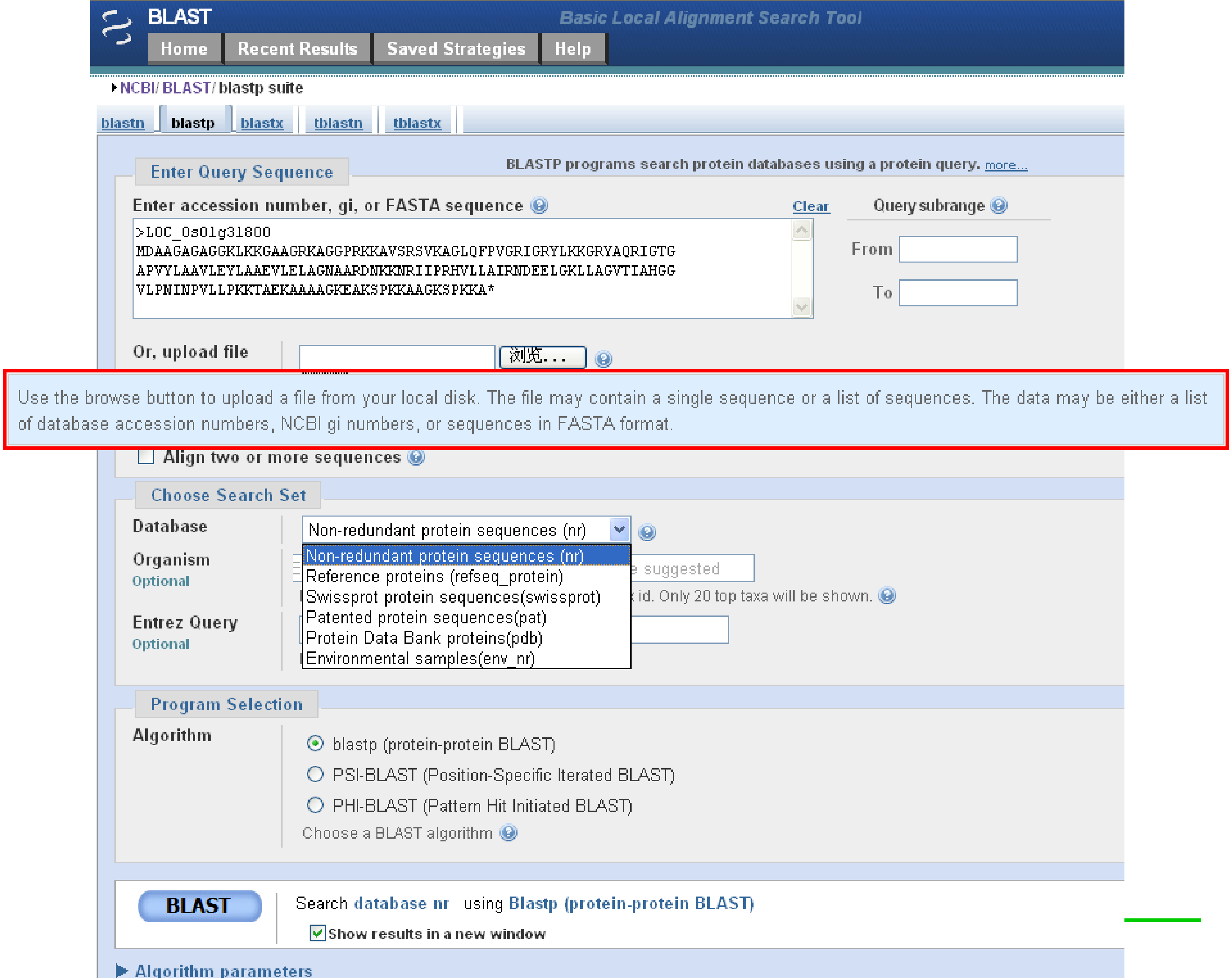
blastn-提交核酸序列

blastp-提交蛋白质序列

blastx-提交核酸序列

tblastn-提交蛋白质序列

tblastx-提交核酸序列


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blastn
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blastx
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tblastx
Enter Query Sequence
BLASTP programs search protein databases using a protein query. more...
Enter accession number, gi, or FASTA sequence
Clear
Query subrange
>LOC_Os01g31800
MDAAGAGAGGKLKKGAAGRKAGGPRKKAVSRSVKAGLQFPVGRIGRYLKKGRYAQRIGTG
APVYLAAVLEYLAAEVLELAGNAARDNKKNRIIPRHVLLAIRNDEELGKLLAGVTIAHGG
VLPNINPVLLPKKTAEKAAAAGKEAKSPKKAAGKSPKKA*
From
To
Or, upload file
浏览...
Use the browse button to upload a file from your local disk. The file may contain a single sequence or a list of sequences. The data may be either a list of database accession numbers, NCBI gi numbers, or sequences in FASTA format.
Align two or more sequences
Choose Search Set
Database
Non-redundant protein sequences (nr)
Non-redundant protein sequences (nr)
Reference proteins (refseq_protein)
Swissprot protein sequences(swissprot)
Patented protein sequences(pat)
Protein Data Bank proteins(pdb)
Environmental samples(env_nr)
Organism
Optional
suggested
id. Only 20 top taxa will be shown.
Entrez Query
Optional
Program Selection
Algorithm
blastp (protein-protein BLAST)
PSI-BLAST (Position-Specific Iterated BLAST)
PHI-BLAST (Pattern Hit Initiated BLAST)
Choose a BLAST algorithm
BLAST
Search database nr using Blastp (protein-protein BLAST)
Show results in a new window
Algorithm parameters

BLAST Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - Y935AKHG01R

Edit and Resubmit | Save Search Strategies | Formatting options | Download

LOC_Os01g31800 (160 letters)

Query ID	lcl|43352
Description	LOC_Os01g31800
Molecule type	amino acid
Query Length	160

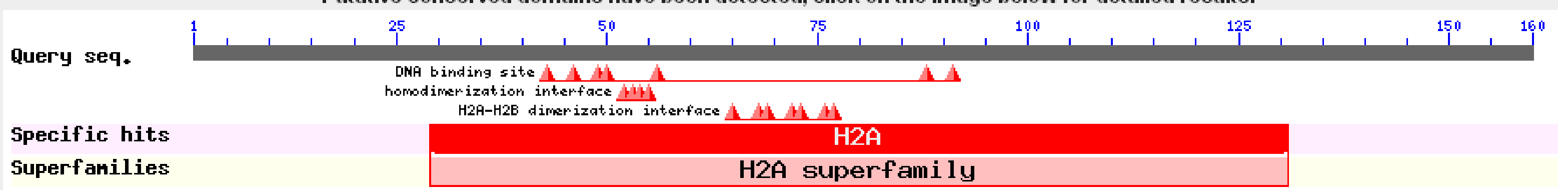
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.2.20+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

Graphic Summary

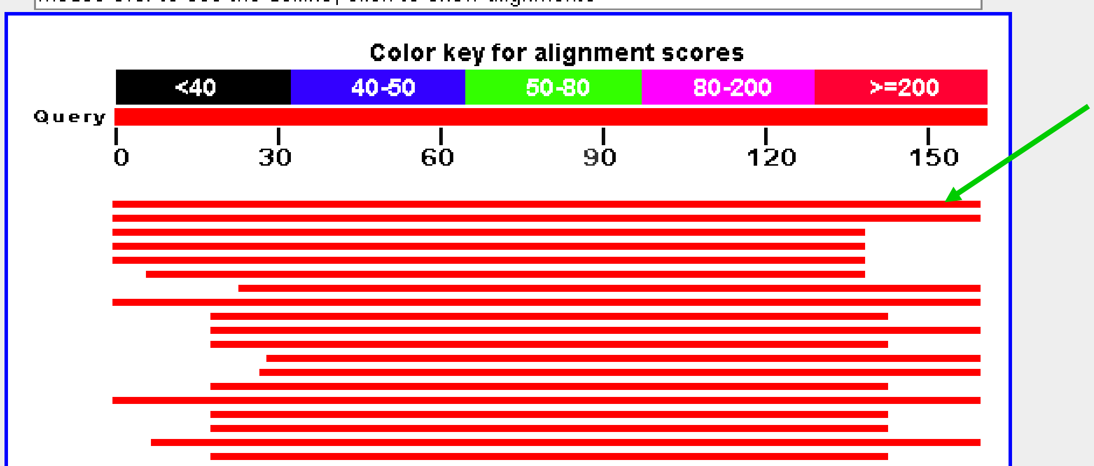
Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



▽ Descriptions

```
Sequences producing significant alignments:                          Score     E
                                                                     (Bits)   Value

ref|NP_001043136.1|  Os01g0502700 [Oryza sativa (japonica cult...    301      1e-80  UG
gb|ACG24512.1|  histone H2A [Zea mays] >gb|ACG24696.1| histone...    259      7e-68
```

▽ Alignments ☐ Select All Get selected sequences Distance tree of results

```
>☐ref|NP_001043136.1| UG Os01g0502700 [Oryza sativa (japonica cultivar-group)]
 ref|NP_001049731.1| G Os03g0279200 [Oryza sativa (japonica cultivar-group)]
 sp|Q94E96.1|H2A5_ORYSJ G RecName: Full=Probable histone H2A.5
 ▷10 more sequence titles
 Length=159

 GENE ID: 4324481 Os01g0502700 | Os01g0502700 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

 Score =  301 bits (771),  Expect = 1e-80, Method: Compositional matrix adjust.
 Identities = 159/159 (100%), Positives = 159/159 (100%), Gaps = 0/159 (0%)

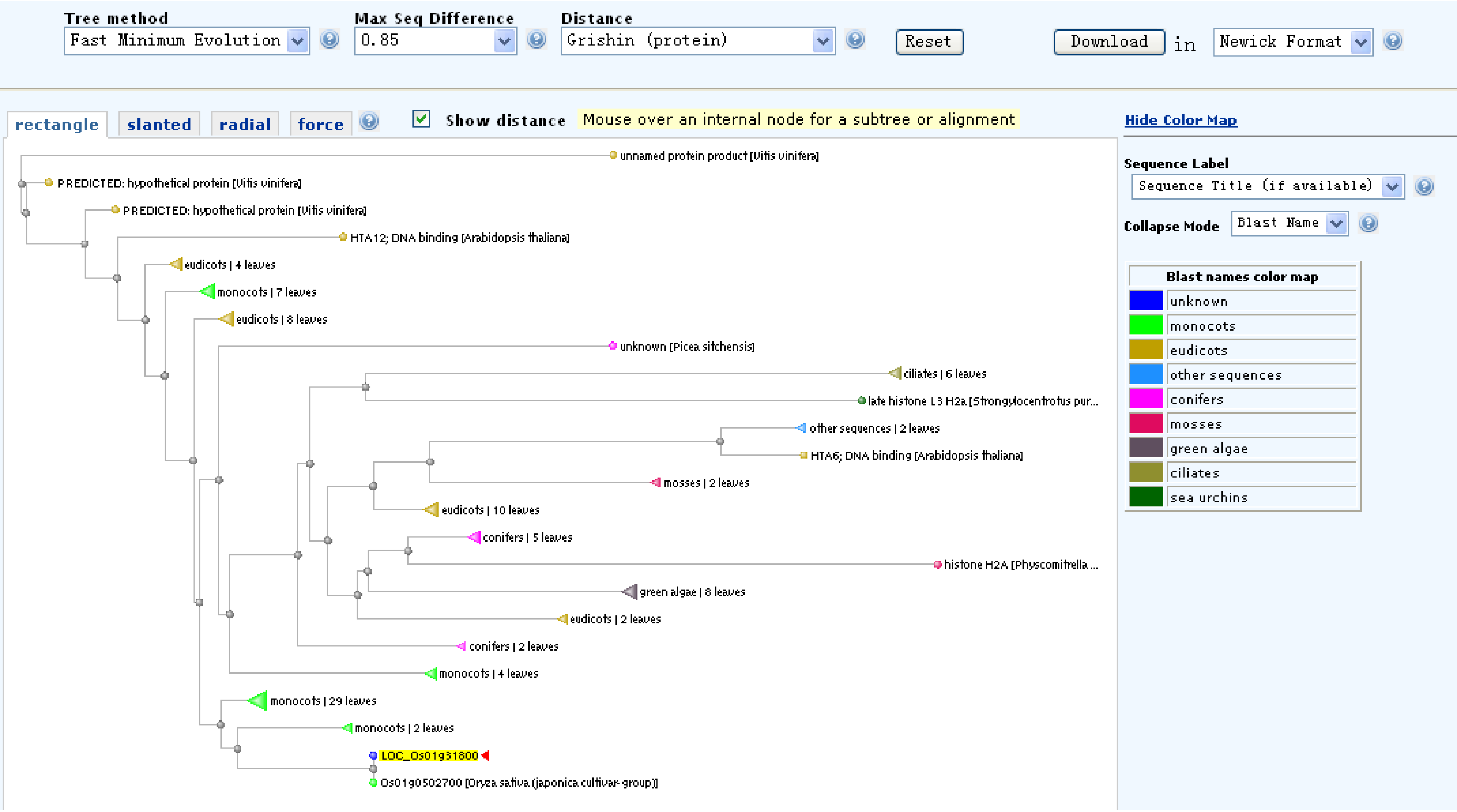
Query  1    MDAAGAGAGGKLKKGAAGRKAGGPRKKAVSRSVKAGLQFPVGRIGRYLKKGRYAQRIGTG  60
            MDAAGAGAGGKLKKGAAGRKAGGPRKKAVSRSVKAGLQFPVGRIGRYLKKGRYAQRIGTG
Sbjct  1    MDAAGAGAGGKLKKGAAGRKAGGPRKKAVSRSVKAGLQFPVGRIGRYLKKGRYAQRIGTG  60

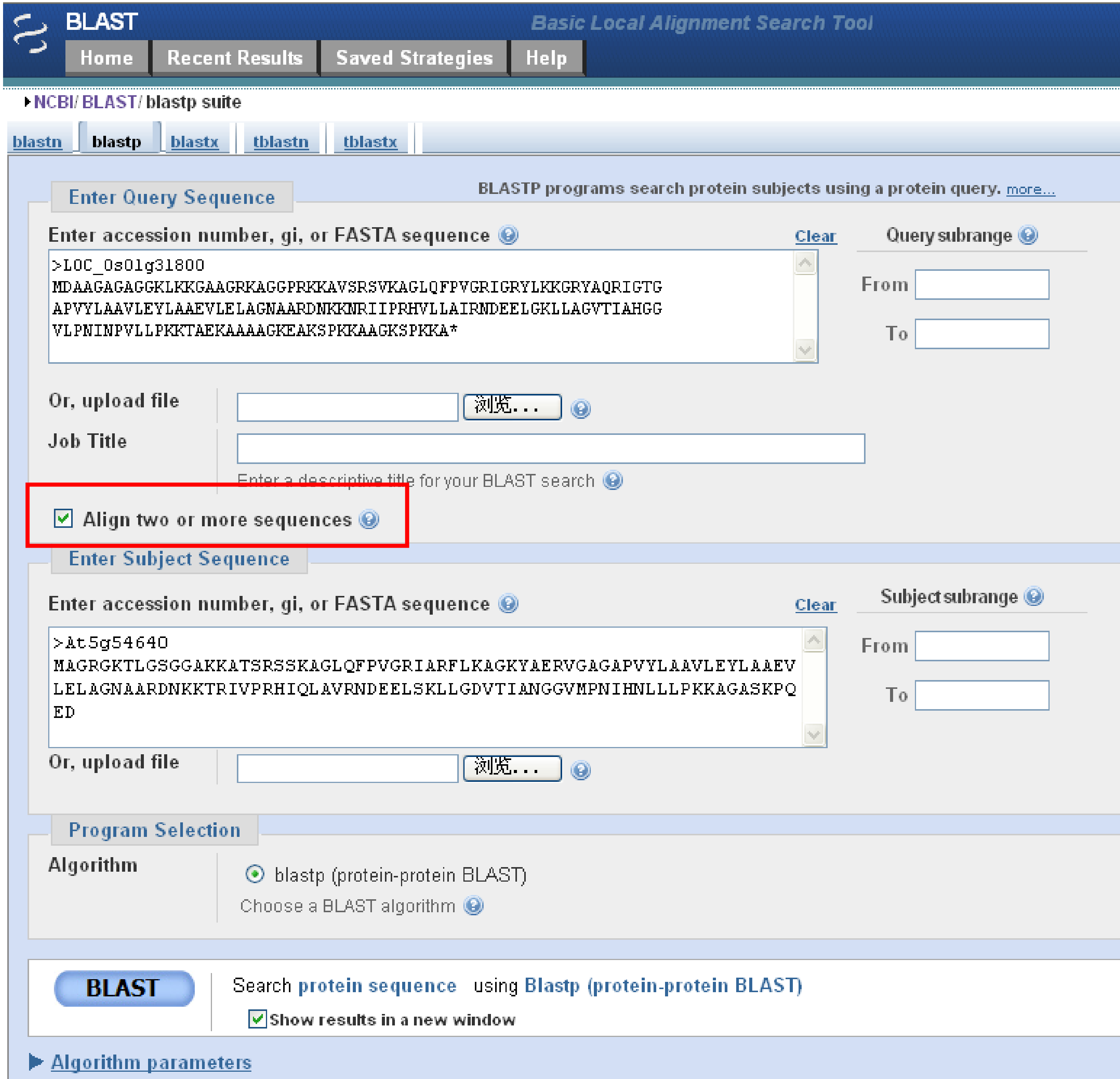
Query  61   APVYLAAVLEYLAAEVLELAGNAARDNKKNRIIPRHVLLAIRNDEELGKLLAGVTIAHGG  120
            APVYLAAVLEYLAAEVLELAGNAARDNKKNRIIPRHVLLAIRNDEELGKLLAGVTIAHGG
Sbjct  61   APVYLAAVLEYLAAEVLELAGNAARDNKKNRIIPRHVLLAIRNDEELGKLLAGVTIAHGG  120

Query  121  VLPNINPVLLPKKTAEKAAAAGKEAKSPKKAAGKSPKKA  159
            VLPNINPVLLPKKTAEKAAAAGKEAKSPKKAAGKSPKKA
Sbjct  121  VLPNINPVLLPKKTAEKAAAAGKEAKSPKKAAGKSPKKA  159


>☐gb|ACG24512.1|  histone H2A [Zea mays]
 gb|ACG24696.1|  histone H2A [Zea mays]
Length=157

 Score =  259 bits (661),  Expect = 7e-68, Method: Compositional matrix adjust.
 Identities = 141/160 (88%), Positives = 149/160 (93%), Gaps = 4/160 (2%)
```


Tree method
Fast Minimum Evolution
Max Seq Difference
0.85
Distance
Grishin (protein)
Reset
Download
in
Newick Format
rectangle
slanted
radial
force
Show distance
Mouse over an internal node for a subtree or alignment
Hide Color Map
unnamed protein product [Vitis vinifera]
PREDICTED: hypothetical protein [Vitis vinifera]
PREDICTED: hypothetical protein [Vitis vinifera]
HTA12; DNA binding [Arabidopsis thaliana]
eudicots | 4 leaves
monocots | 7 leaves
eudicots | 8 leaves
unknown [Picea sitchensis]
ciliates | 6 leaves
late histone L3 H2a [Strongylocentrotus pur...
other sequences | 2 leaves
HTA6; DNA binding [Arabidopsis thaliana]
mosses | 2 leaves
eudicots | 10 leaves
conifers | 5 leaves
histone H2A [Physcomitrella ...
green algae | 8 leaves
eudicots | 2 leaves
conifers | 2 leaves
monocots | 4 leaves
monocots | 29 leaves
monocots | 2 leaves
LOC_Os01g31800
Os01g0502700 [Oryza sativa (japonica cultivar-group)]
Sequence Label
Sequence Title (if available)
Collapse Mode
Blast Name
Blast names color map
unknown
monocots
eudicots
other sequences
conifers
mosses
green algae
ciliates
sea urchins


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Home
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Saved Strategies
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blastx
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tblastx
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BLASTP programs search protein subjects using a protein query. more...
Enter accession number, gi, or FASTA sequence
Clear
Query subrange
>LOC_Os01g31800
MDAAGAGAGGKLKKGAAGRKAGGPRKKAVSRSVKAGLQFPVGRIGRYLKKGRYAQRIGTG
APVYLAAVLEYLAAEVLELAGNAARDNKKNRIIPRHVLLAIRNDEELGKLLAGVTIAHGG
VLPNINPVLLPKKTAEKAAAAGKEAKSPKKAAGKSPKKA*
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Align two or more sequences
Enter Subject Sequence
Enter accession number, gi, or FASTA sequence
Clear
Subject subrange
>At5g54640
MAGRGKTLGSGGAKKATSRSSKAGLQFPVGRIARFLKAGKYAERVGAGAPVYLAAVLEYLAAEV
LELAGNAARDNKKTRIVPRHIQLAVRNDEELSKLLGDVTIANGGVMPNIHNLLLPKKAGASKPQ
ED
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blastp (protein-protein BLAST)
Choose a BLAST algorithm
BLAST
Search protein sequence using Blastp (protein-protein BLAST)
Show results in a new window
Algorithm parameters

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Blast 2 sequences

LOC_Os01g31800 (160 letters)

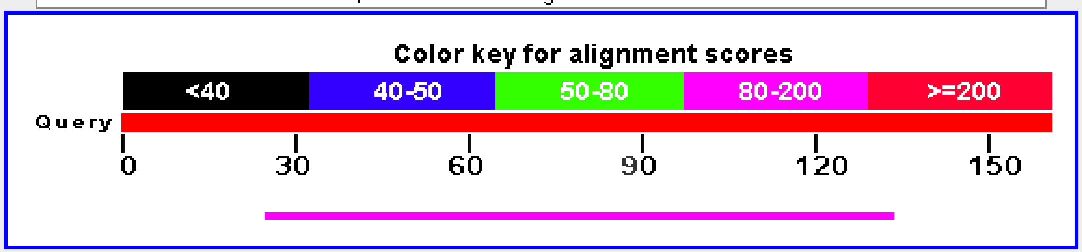
Query ID	lcl|59405	**Subject ID**	59407
Description	LOC_Os01g31800	**Description**	At5g54640
Molecule type	amino acid	**Molecule type**	amino acid
Query Length	160	**Subject Length**	130
		Program	BLASTP 2.2.20+ Citation

Other reports: Search Summary [Taxonomy reports]

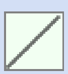
Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



Dot Matrix View



Descriptions

```
                                                                  Score     E
Sequences producing significant alignments:                      (Bits)   Value

lcl|59407  At5g54640                                               177    4e-50
```

Alignments

Select All   Get selected sequences   Distance tree of results

```
>lcl|59407 At5g54640
Length=130

 Score =  177 bits (450),  Expect = 4e-50, Method: Compositional matrix adjust.
 Identities = 86/108 (79%), Positives = 97/108 (89%), Gaps = 0/108 (0%)

Query  26   KKAVSRSVKAGLQFPVGRIGRYLKKGRYAQRIGTGAPVYLAAVLEYLAAEVLELAGNAAR  85
            KKA SRS KAGLQFPVGRI R+LK G+YA+R+G GAPVYLAAVLEYLAAEVLELAGNAAR
Sbjct  14   KKATSRSSKAGLQFPVGRIARFLKAGKYAERVGAGAPVYLAAVLEYLAAEVLELAGNAAR  73

Query  86   DNKKNRIIPRHVLLAIRNDEELGKLLAGVTIAHGGVLPNINPVLLPKK  133
            DNKK RI+PRH+ LA+RNDEEL KLL  VTIA+GGV+PNI+ +LLPKK
Sbjct  74   DNKKTRIVPRHIQLAVRNDEELSKLLGDVTIANGGVMPNIHNLLLPKK  121
```

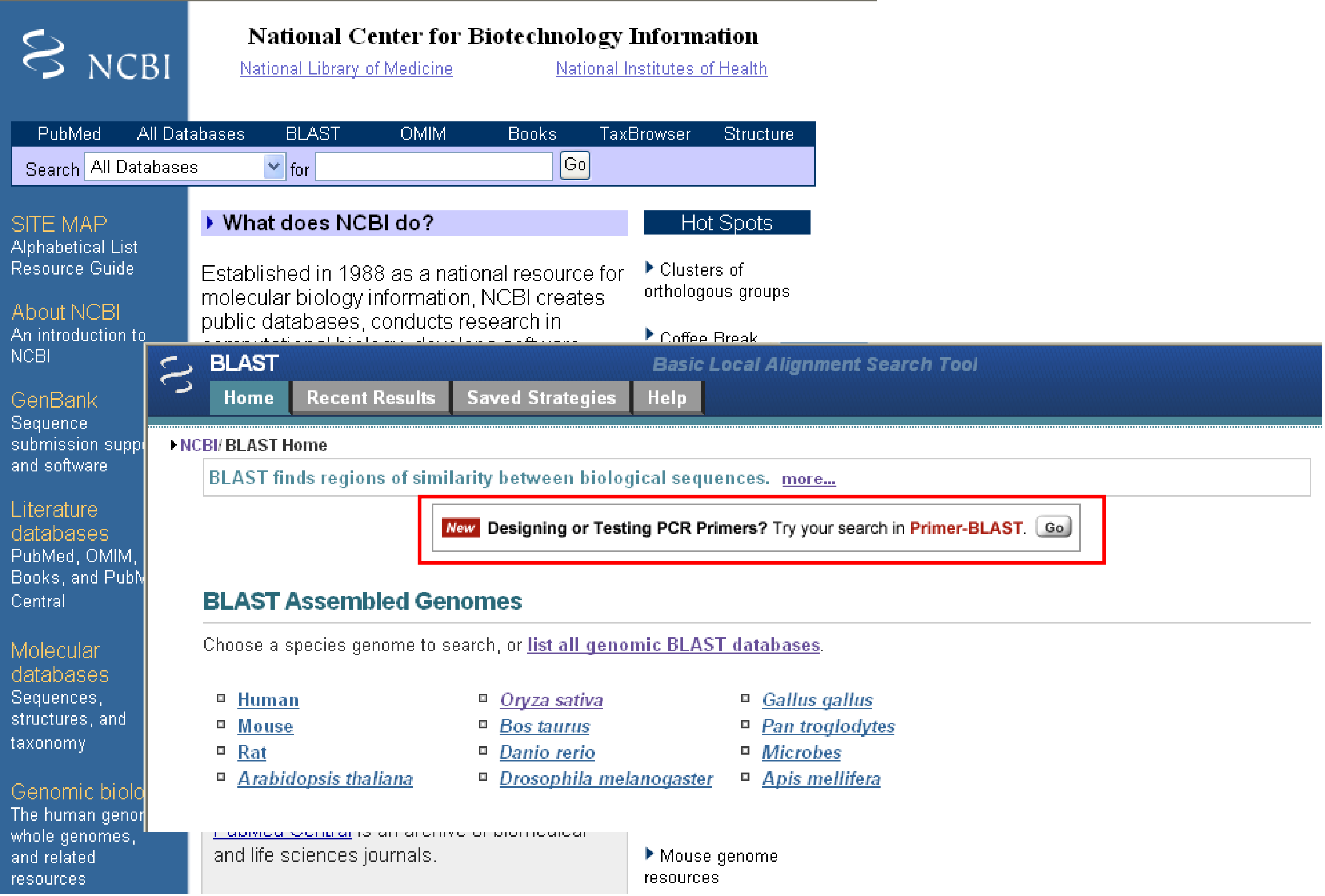
Select All   Get selected sequences   Distance tree of results

Blast- Specialized BLAST

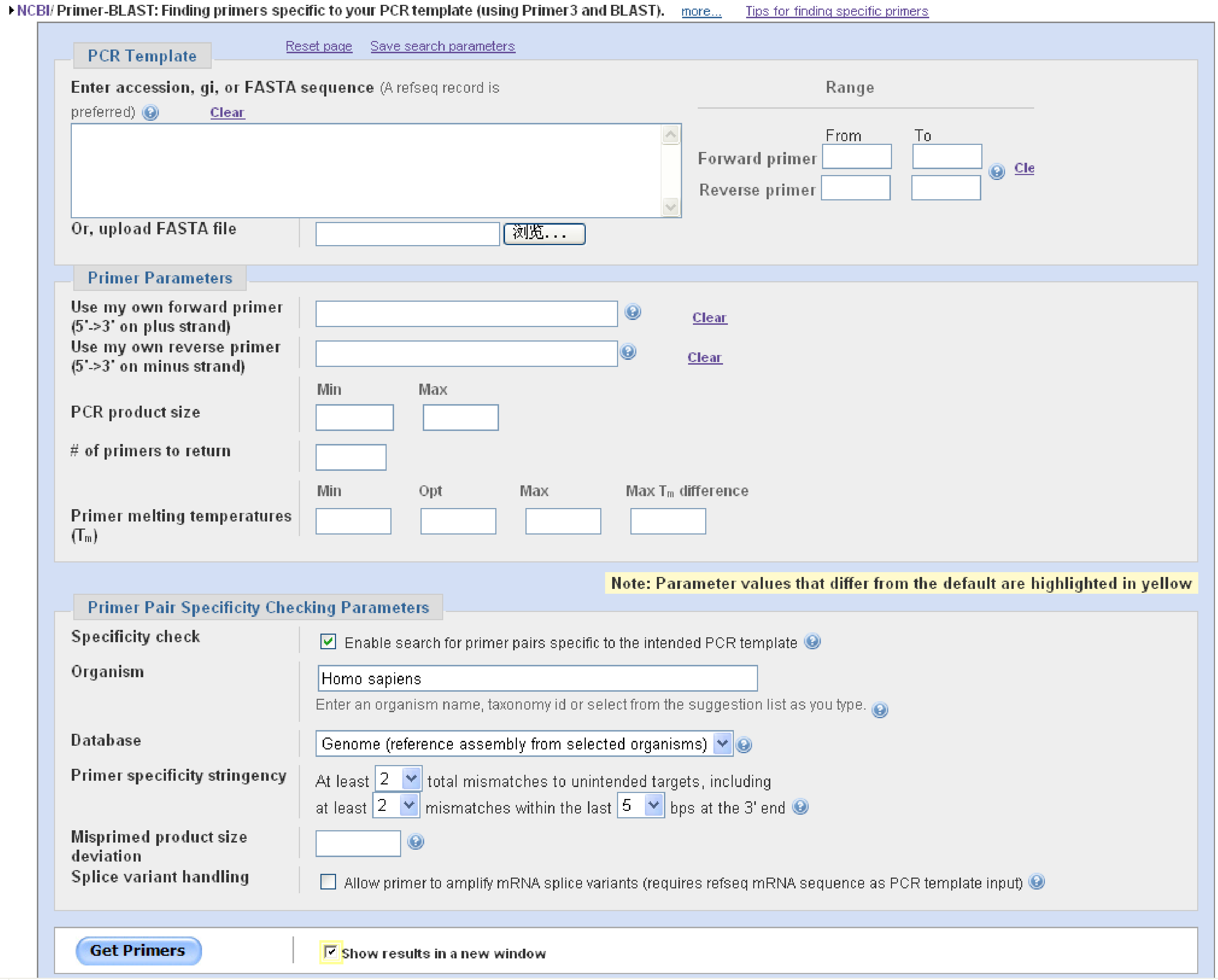
Specialized BLAST

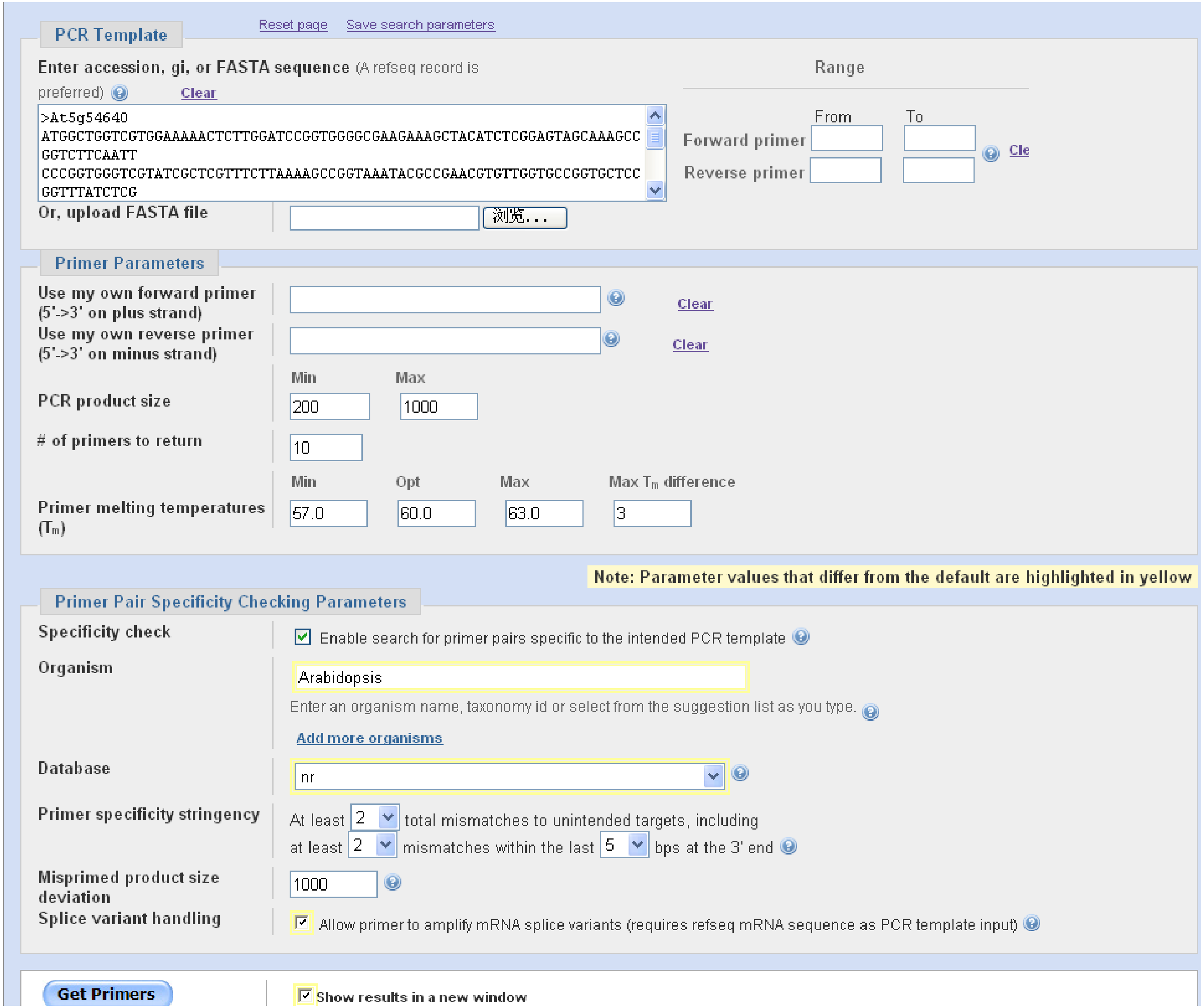
Choose a type of specialized search (or database name in parentheses.)

- Make specific primers with Primer-BLAST
- Search trace archives
- Find conserved domains in your sequence (cds)
- Find sequences with similar conserved domain architecture (cdart)
- Search sequences that have gene expression profiles (GEO)
- Search immunoglobulins (IgBLAST)
- Search for SNPs (snp)
- Screen sequence for vector contamination (vecscreen)
- Align two (or more) sequences using BLAST (bl2seq)
- Search protein or nucleotide targets in PubChem BioAssay
- Search SRA transcript libraries


NCBI
National Center for Biotechnology Information
National Library of Medicine
National Institutes of Health
PubMed All Databases BLAST OMIM Books TaxBrowser Structure
Search All Databases for Go
SITE MAP
Alphabetical List
Resource Guide
About NCBI
An introduction to NCBI
GenBank
Sequence
and software
Literature databases
PubMed, OMIM,
Central
Molecular databases
Sequences, structures, and taxonomy
whole genomes,
and related resources
What does NCBI do?
Established in 1988 as a national resource for molecular biology information, NCBI creates public databases, conducts research in
and life sciences journals.
Hot Spots
Clusters of orthologous groups
Mouse genome resources
BLAST
Basic Local Alignment Search Tool
Home
Recent Results
Saved Strategies
Help
NCBI/ BLAST Home
BLAST finds regions of similarity between biological sequences. more...
New Designing or Testing PCR Primers? Try your search in Primer-BLAST. Go
BLAST Assembled Genomes
Choose a species genome to search, or list all genomic BLAST databases.
Human
Mouse
Rat
Arabidopsis thaliana
Oryza sativa
Bos taurus
Danio rerio
Drosophila melanogaster
Gallus gallus
Pan troglodytes
Microbes
Apis mellifera

Blast- Primer-BLAST



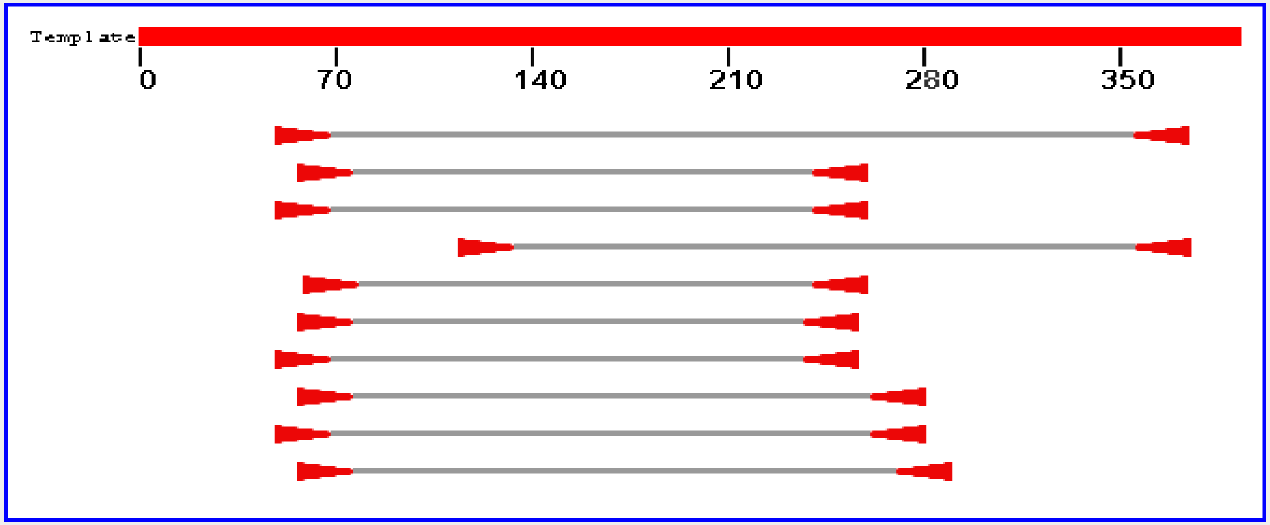

PCR Template
Reset page
Save search parameters
Enter accession, gi, or FASTA sequence (A refseq record is preferred)
Clear
>At5g54640
ATGGCTGGTCGTGGAAAAACTCTTGGATCCGGTGGGGCGAAGAAAGCTACATCTCGGAGTAGCAAAGCC
GGTCTTCAATT
CCCGGTGGGTCGTATCGCTCGTTTCTTAAAAGCCGGTAAATACGCCGAACGTGTTGGTGCCGGTGCTCC
GGTTTATCTCG
Range
From
To
Forward primer
Reverse primer
Cle
Or, upload FASTA file
浏览...
Primer Parameters
Use my own forward primer (5'->3' on plus strand)
Clear
Use my own reverse primer (5'->3' on minus strand)
Clear
Min
Max
PCR product size
200
1000
of primers to return
10
Min
Opt
Max
Max Tm difference
Primer melting temperatures (Tm)
57.0
60.0
63.0
3
Note: Parameter values that differ from the default are highlighted in yellow
Primer Pair Specificity Checking Parameters
Specificity check
Enable search for primer pairs specific to the intended PCR template
Organism
Arabidopsis
Enter an organism name, taxonomy id or select from the suggestion list as you type.
Add more organisms
Database
nr
Primer specificity stringency
At least 2 total mismatches to unintended targets, including
at least 2 mismatches within the last 5 bps at the 3' end
Misprimed product size deviation
1000
Splice variant handling
Allow primer to amplify mRNA splice variants (requires refseq mRNA sequence as PCR template input)
Get Primers
Show results in a new window

Primer-BLAST Primer designing tool

NCBI/ Primer-BLAST : results more...

Input PCR template At5g54640
Range 1 - 393
Specificity of primers primers may not be specific to the input PCR template as targets were found in selected database:All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences) (Organism limited to Arabidopsis)

Summary of primer pairs



Detailed primer reports

Detailed primer reports

Primer pair 1

	Sequence (5'->3')	Strand on template	Length	Start	Stop	Tm	GC%
Forward primer	CATCTCGGAGTAGCAAAGCC	Plus	20	50	69	59.98	55.00%
Reverse primer	TTTGAAGCACCAGCCTTCTT	Minus	20	377	358	59.99	45.00%
Product length	328						

Products on potentially unintended templates

>NM_124845.3 Arabidopsis thaliana HTA1/RAT5 (RESISTANT TO AGROBACTERIUM TRANSFORMATION 5); DNA binding (HTA1/RAT5) mRNA, complete cds

```
product length = 328
Forward primer  1    CATCTCGGAGTAGCAAAGCC  20
Template        113  ....................  132

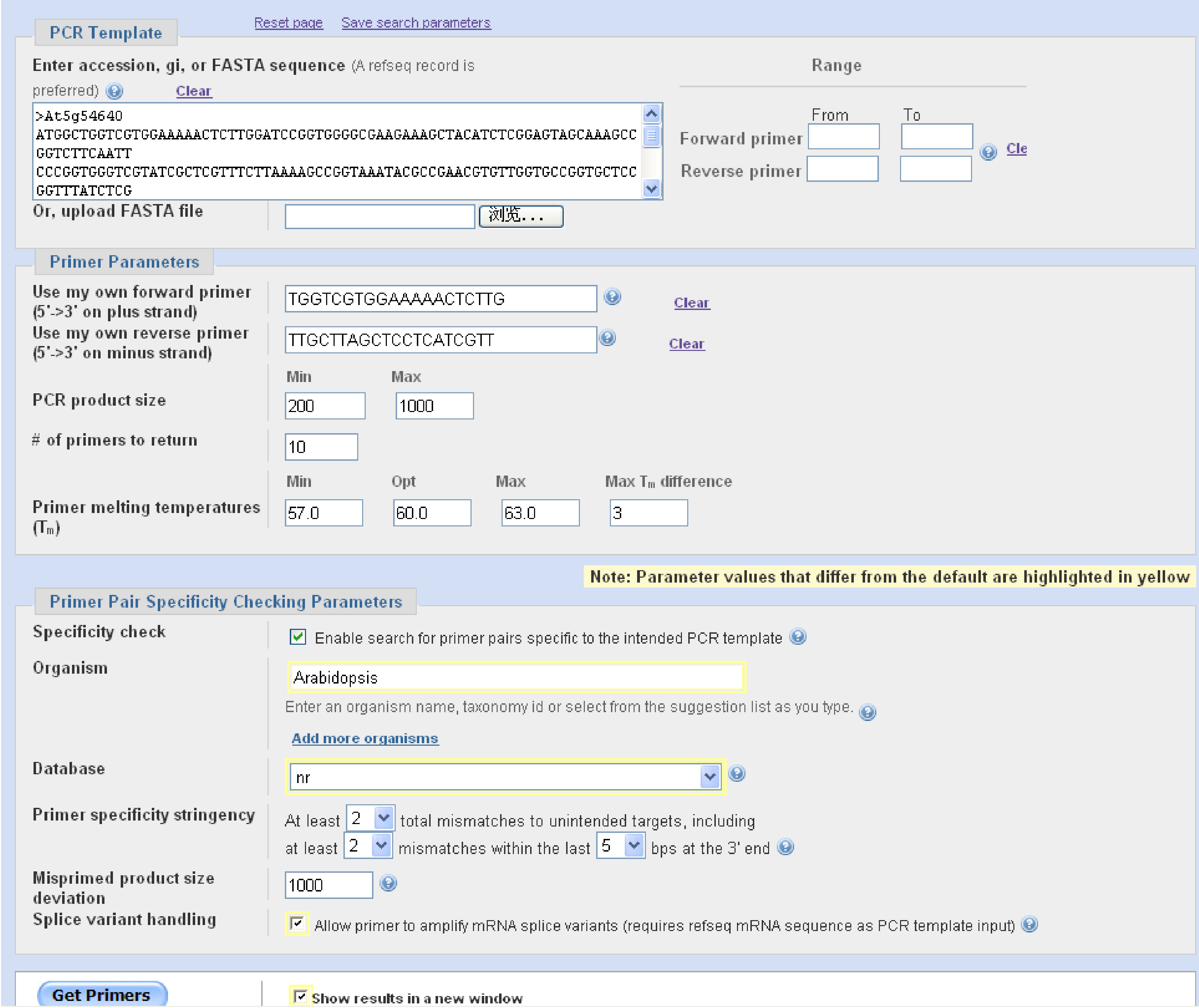
Reverse primer  1    TTTGAAGCACCAGCCTTCTT  20
Template        440  ....................  421
```

>AY088261.1 Arabidopsis thaliana clone 4875 mRNA, complete sequence

```
product length = 328
Forward primer  1    CATCTCGGAGTAGCAAAGCC  20
Template        111  ....................  130

Reverse primer  1    TTTGAAGCACCAGCCTTCTT  20
Template        438  ....................  419
```

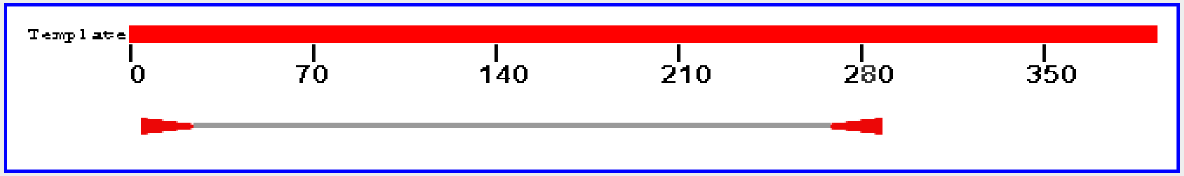
>BT005189.1 Arabidopsis thaliana clone U20557 putative histone H2A protein (At5g54640) mRNA, complete cds


PCR Template
Reset page
Save search parameters
Enter accession, gi, or FASTA sequence (A refseq record is preferred)
Clear
>At5g54640
ATGGCTGGTCGTGGAAAAACTCTTGGATCCGGTGGGGCGAAGAAAGCTACATCTCGGAGTAGCAAAGCC
GGTCTTCAATT
CCCGGTGGGTCGTATCGCTCGTTTCTTAAAAGCCGGTAAATACGCCGAACGTGTTGGTGCCGGTGCTCC
GGTTTATCTCG
Or, upload FASTA file
浏览...
Range
From
To
Forward primer
Reverse primer
Cle
Primer Parameters
Use my own forward primer (5'->3' on plus strand)
TGGTCGTGGAAAAACTCTTG
Clear
Use my own reverse primer (5'->3' on minus strand)
TTGCTTAGCTCCTCATCGTT
Clear
PCR product size
Min
Max
200
1000
of primers to return
10
Primer melting temperatures (Tm)
Min
Opt
Max
Max Tm difference
57.0
60.0
63.0
3
Note: Parameter values that differ from the default are highlighted in yellow
Primer Pair Specificity Checking Parameters
Specificity check
Enable search for primer pairs specific to the intended PCR template
Organism
Arabidopsis
Enter an organism name, taxonomy id or select from the suggestion list as you type.
Add more organisms
Database
nr
Primer specificity stringency
At least 2 total mismatches to unintended targets, including
at least 2 mismatches within the last 5 bps at the 3' end
Misprimed product size deviation
1000
Splice variant handling
Allow primer to amplify mRNA splice variants (requires refseq mRNA sequence as PCR template input)
Get Primers
Show results in a new window

NCBI/ Primer-BLAST : results more...

Input PCR template	At5g54640
Range	1 - 393
Specificity of primers	primers may not be specific to the input PCR template as targets were found in selected database:All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences) (Organism limited to Arabidopsis)

Summary of primer pairs



Detailed primer reports

Primer pair 1

	Sequence (5'->3')	Strand on template	Length	Start	Stop	Tm	GC%
Forward primer	TGGTCGTGGAAAAACTCTTG	Plus	20	6	25	58.75	45.00%
Reverse primer	TTGCTTAGCTCCTCATCGTT	Minus	20	290	271	57.73	45.00%
Product length	285						

Products on potentially unintended templates

>NM_124845.3 Arabidopsis thaliana HTA1/RAT5 (RESISTANT TO AGROBACTERIUM TRANSFORMATION 5); DNA binding (HTA1/RAT5) mRNA, complete cds

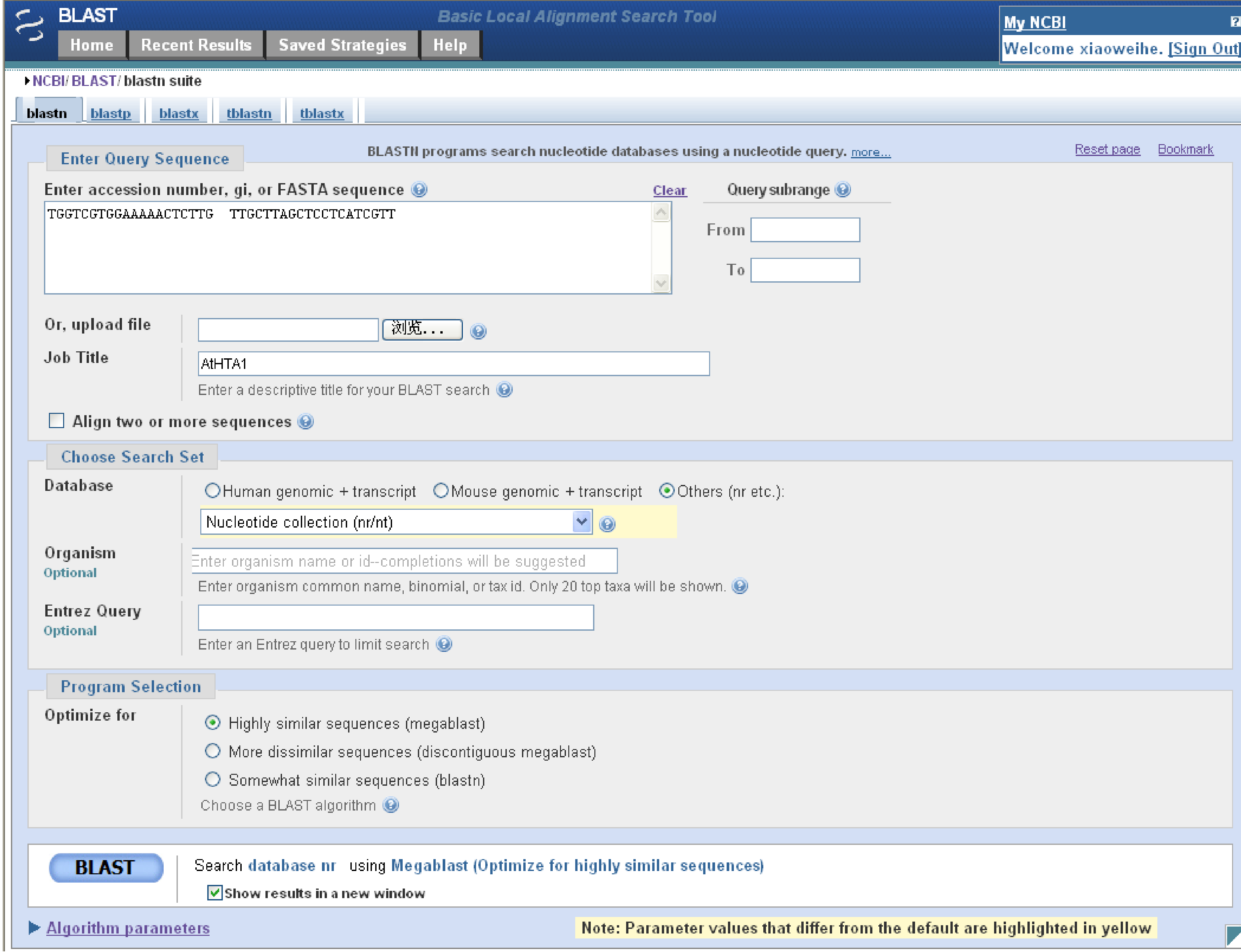
```
product length = 285
Forward primer  1    TGGTCGTGGAAAAACTCTTG  20
Template        69   ....................  88

Reverse primer  1     TTGCTTAGCTCCTCATCGTT  20
Template        353   ....................  334
```

>AY088261.1 Arabidopsis thaliana clone 4875 mRNA, complete sequence

其他Primer专业设计软件

- **Oligo**
- **Primer Primer**
- **Vector NT**
- **DNAstar**
- 一些网络资源：
  - 麻省理工学院 ***http://frodo.wi.mit.edu/***
  - 斯坦福大学 ***http://seq.yeastgenome.org/cgi-bin/web-primer***


BLAST
Basic Local Alignment Search Tool
Home
Recent Results
Saved Strategies
Help
My NCBI
Welcome xiaoweihe. [Sign Out]
NCBI/ BLAST/ blastn suite
blastn
blastp
blastx
tblastn
tblastx
Enter Query Sequence
BLASTN programs search nucleotide databases using a nucleotide query. more...
Reset page
Bookmark
Enter accession number, gi, or FASTA sequence
Clear
TGGTCGTGGAAAAACTCTTG TTGCTTAGCTCCTCATCGTT
Query subrange
From
To
Or, upload file
浏览...
Job Title
AtHTA1
Enter a descriptive title for your BLAST search
Align two or more sequences
Choose Search Set
Database
Human genomic + transcript
Mouse genomic + transcript
Others (nr etc.):
Nucleotide collection (nr/nt)
Organism
Optional
Enter organism name or id--completions will be suggested
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.
Entrez Query
Optional
Enter an Entrez query to limit search
Program Selection
Optimize for
Highly similar sequences (megablast)
More dissimilar sequences (discontiguous megablast)
Somewhat similar sequences (blastn)
Choose a BLAST algorithm
BLAST
Search database nr using Megablast (Optimize for highly similar sequences)
Show results in a new window
Algorithm parameters
Note: Parameter values that differ from the default are highlighted in yellow

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

AtHTA1

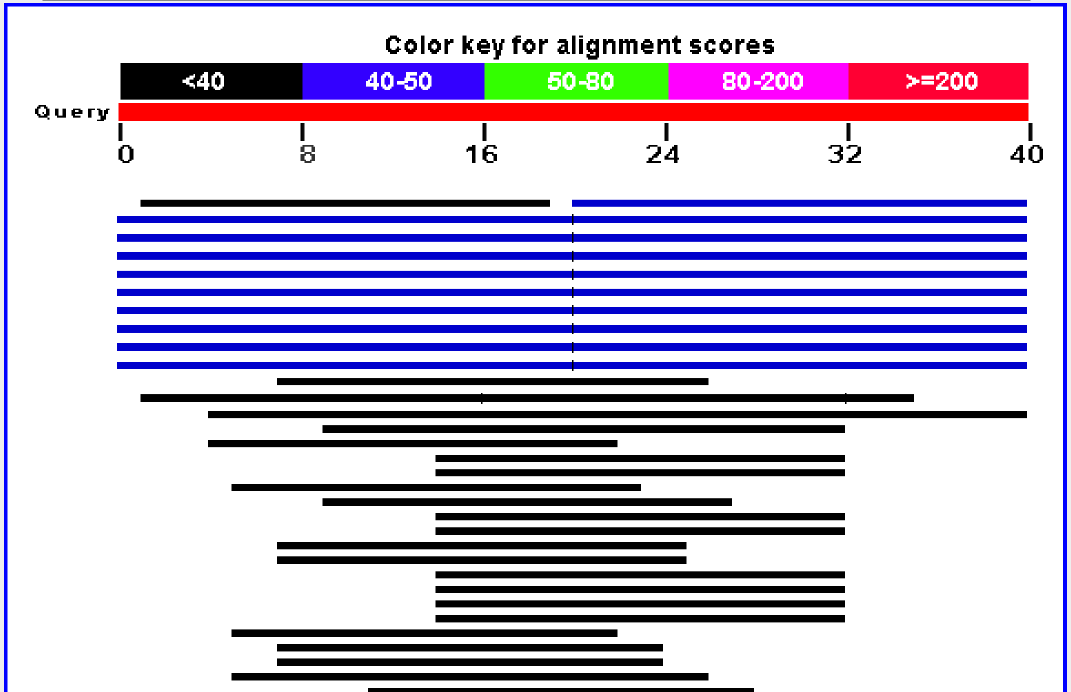
Query ID	lcl|25805	**Database Name**	nr
Description	None	**Description**	All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
Molecule type	nucleic acid	**Program**	BLASTN 2.2.20+ Citation
Query Length	40		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

Graphic Summary

Distribution of 118 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments



▽ Descriptions

Legend for links to other resources: U UniGene E GEO G Gene S Structure M Map Viewer

▽ Alignments Select All Get selected sequences Distance tree of results

```
>ref|XM_002328499.1| G Populus trichocarpa histone 2 (HTA909), mRNA
Length=660

 GENE ID: 7481104 HTA909 | histone 2 [Populus trichocarpa]
(10 or fewer PubMed links)

 Score = 40.1 bits (20),  Expect = 0.44
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

Query  21   TTGCTTAGCTCCTCATCGTT  40
            ||||||||||||||||||||
Sbjct  370  TTGCTTAGCTCCTCATCGTT  351


>ref|NM_124845.3| UEG Arabidopsis thaliana HTA1/RAT5 (RESISTANT TO AGROBACTERIUM TRANSFORMATION
5); DNA binding (HTA1/RAT5) mRNA, complete cds
Length=669

 GENE ID: 835553 HTA1/RAT5 | HTA1/RAT5 (RESISTANT TO AGROBACTERIUM
TRANSFORMATION 5); DNA binding [Arabidopsis thaliana] (10 or fewer PubMed links)

                                                  Sort alignments for this subject sequence by:
                                                    E value  Score  Percent identity
                                                    Query start position  Subject start position

 Score = 40.1 bits (20),  Expect = 0.44
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Plus

Query  1   TGGTCGTGGAAAAACTCTTG  20
           ||||||||||||||||||||
Sbjct  69  TGGTCGTGGAAAAACTCTTG  88


 Score = 40.1 bits (20),  Expect = 0.44
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

Query  21   TTGCTTAGCTCCTCATCGTT  40
            ||||||||||||||||||||
Sbjct  353  TTGCTTAGCTCCTCATCGTT  334
```

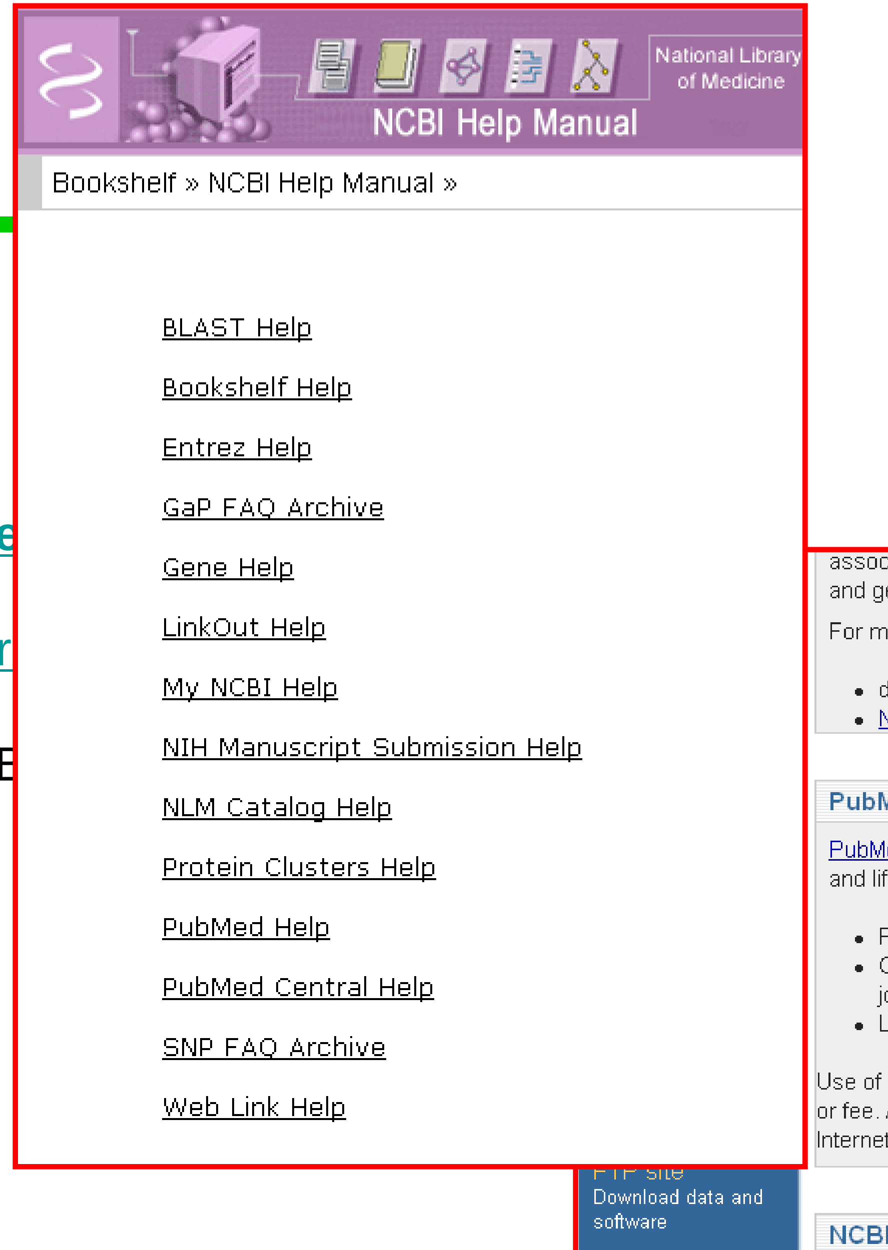
Question?

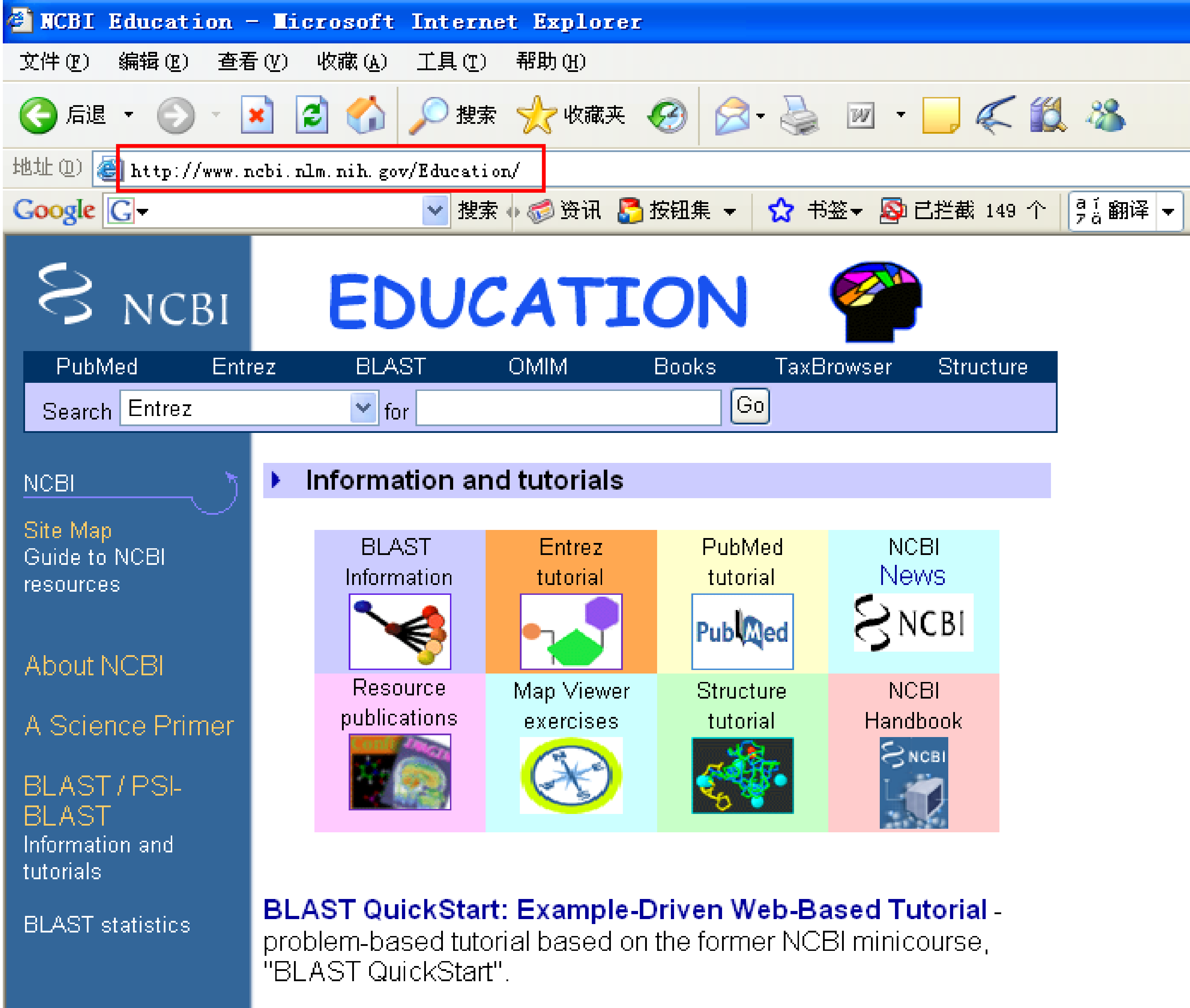
- Email to xwhe@lib.zju.edu.cn
- See the NCBI Help chapter **Bookshe**

http://www.ncbi.nlm.nih.gov/bookshelf/br

- See the Education Section of the NCE

http://www.ncbi.nlm.nih.gov/Education/




NCBI Education - Microsoft Internet Explorer
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后退
搜索
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http://www.ncbi.nlm.nih.gov/Education/
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搜索
资讯
按钮集
书签
已拦截 149 个
翻译
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PubMed
Entrez
BLAST
OMIM
Books
TaxBrowser
Structure
Search
Entrez
for
Go
NCBI
Site Map
Guide to NCBI resources
About NCBI
A Science Primer
BLAST / PSI-BLAST
Information and tutorials
BLAST statistics
Information and tutorials
BLAST Information
Entrez tutorial
PubMed tutorial
NCBI News
Resource publications
Map Viewer exercises
Structure tutorial
NCBI Handbook
BLAST QuickStart: Example-Driven Web-Based Tutorial -
problem-based tutorial based on the former NCBI minicourse, "BLAST QuickStart".

Thanks！



